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(54) Title: HIGH THROUGHPUT MULTIPLEX DNA SEQUENCE AMPLIFICATIONS

Criteria Used in Designing Primers That Are Experimentally Acceptable	
Tm Range of the primers (°C)	75-103
Length of the primers (bp)	24-33
Number of consecutive matching bases between the 3' ends of any two primer molecules	<4
Number of consecutive matching bases with one mismatch between the 3'-ends of any two primer molecules	<7
Number of consecutive matching bases between the 3'-end of one primer molecule and anywhere in another primer molecule	<9
Number of consecutive matching bases with one mismatch between the 3'-end of one primer molecule and anywhere in another primer molecule	<11
Maximal number of matching bases between two primer molecules	<75%
Number of consecutive matching bases between the 3'-end a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	12
Number of consecutive matching bases with one mismatch between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	15
Maximal number of matching bases between a primer molecule and a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	<80%

(57) Abstract: The present invention provides methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments. The present invention allows a multiplex PCR to use at least 50 pairs of primers and produce at least 50 DNA fragments of interest. The present invention significantly broadens the application of multiplex PCR in the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, the gene expression profiling in various samples, and high throughput genotyping technologies.

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High Throughput Multiplex DNA Sequence AmplificationsReference to Government Grant

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5 by the National Human Genome Research Institute. The U.S. government may have certain  
rights in this invention.

Field of the Invention

This invention pertains to the field of high throughput multiplex DNA sequence  
amplification. Specifically, the invention pertains to methods of designing primers that allow  
10 the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase  
chain reaction and minimize the formation of nonspecific extension of undesired DNA  
fragments.

Background

The polymerase chain reaction (PCR) is a primer-directed *in vitro* reaction for the  
15 enzymatic amplification of a specific DNA fragment. Saiki, Enzymatic Amplification of  $\beta$ -  
Actin Genomic Sequences and Restriction Site Analysis for Diagnosis of Sickle Cell Anemia,  
*Science* 230: 1350-54 (1985). The PCR process is involved in the repetitive cycles of  
denaturation, primer annealing and extension by a thermostable DNA polymerase of two  
oligonucleotide primers that flank the DNA region of interest in a template DNA sample. At  
20 the beginning the PCR process, the duplex DNA target is denatured into two separated  
strands of DNA through a first heating step. In a subsequent annealing step, each  
oligonucleotide primer anneals or hybridizes to the complementary sequence of one separated  
strand of the target DNA. In a third extension step, nascent DNA is synthesized by extending

each primer from its 3' hydroxyl end of towards the 5' end of the annealed target DNA strand by a thermostable DNA polymerase. The heating or denaturation step, the primer annealing step and the enzymatic extension step together constitute a single PCR cycle. If the newly synthesized DNA strand extends to or beyond the region complementary to the other primer, it serves as a primer annealing site and a template for extension in a subsequent PCR cycle. As a result, the repetitive PCR cycles give rise to the exponential accumulation of a specific DNA fragment whose termini are defined by the 5' ends of the two primers. Theoretically, at the  $n$ th cycle of the PCR process, a single DNA molecule can produce  $2^n$  progeny DNA fragments of interest.

The distinctive nature of the PCR process in producing a substantive quantity of DNA fragments of interest from an initial tiny amount of DNA sample has gained broad applications in the field of biomedical research and clinical diagnosis. For example, PCR has been widely used in the diagnosis of inherited disorder and the individualization of evidence samples in the forensics area. Erlich *et al*, Recent Advances in the Polymerase Chain Reaction, *Science* 252: 1643-51 (1991); Newton & Graham, PCR (Oxford, 1994). In particular, PCR has played a critical role in genotyping a vast number of genetic polymorphisms and individual variations which underlie the onset of many diseases. Shi, Enabling Large-Scale Pharmacogenetic Studies by High-throughput Mutation Detection and Genotyping Technologies, *Clin. Chem.* 47: 164-172 (2001).

Widespread applications notwithstanding, the use of PCR is quite often limited by cost, time, and the availability of adequate test samples. To illustrate, the human genome project has placed over 6000 DNA markers in human genetic mapping. To analysis these 6000 markers in 1000 specimens, a total of 6,000,000 PCR reactions are needed if only one

marker sequence is amplified in each reaction. As a well equipped laboratory may process 300 reactions and post-PCR assay a day, it will take a total of 20,000 working days or 80 years to complete the analysis, provided that the amount of each specimen suffices 6000 reactions.

5 In overcoming these limitations, a variant PCR termed multiplex PCR has been developed. Chamberlian *et al*, Deletion Screening of the Duchenne Muscular Dystrophy Locus via Multiplex DNA Amplification, *Nucleic Acids Res.* 16: 11141-56 (1988). Unlike the standard or uniplex PCR where only one pair of primers is used to amplify a single DNA fragment of interest, the multiplex PCR includes more than one pair of primers and thus  
10 results in more than one DNA fragment. Since its inception, the multiplex PCR has been applied in many areas of DNA testing, including gene deletion analysis, Chamberlain, *supra*, mutation and polymorphism analysis, Rithidech *et al*, Combining Multiplex and Touch Down PCR to Screen Murine Microsatellite Polymorphism, *Bio-Techniques* 23: 36-45 (1997), quantitative analysis, Zimmermann *et al*, Quantitative Multiple Competitive PCR of HIV-  
15 DNA in a Single Reaction Tube, *BioTechniques* 21: 480-484 (1996), RNA detection, Zou, Identification of New Influenza B virus Variants by Multiplex Reverse Transcription-PCR and the Heteroduplex Mobility Assay, *J. Clin. Microbiol.* 36: 1544-1548 (1998), and identification of microorganisms, Elnifro *et al*, Multiplex PCR: Optimization and Application in Diagnostic Virology, *Clin. Microbiol. Rev.* 13: 559-570 (2000).

20 Conceptually, the multiplex PCR has the potential to produce considerable savings in cost, time and sample volume. In aforementioned project of analyzing 6000 DNA markers in 1000 specimens, if  $n$  pairs of primers are used in a multiplex PCR reaction, it will only cost one- $n$ th of 20,000 working days to complete the project as well as one- $n$ th of the cost and

sample volume required in the uniplex PCR reactions. Despite the attractive potential, the application of the multiplex PCR poses many challenges. For example, even under carefully optimized reaction conditions, only 26 DNA fragments could be amplified simultaneously in a single multiplex PCR. Edwards & Gibbs, Multiplex PCR: Advantages, Developments and Applications, *PCR Meth. Appl.* 3: S65-75 (1994); Lin *et al*, Multiplex Genotype Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587 (1996).

Researchers are facing two tiers of challenge in optimizing the multiplex PCR. The first tier of challenge is the efficacy of PCR. In general, this issue is ubiquitous in all PCR reactions, whether in multiplex PCR or uniplex PCR. The efficacy of PCR is measured by its specificity, efficiency and fidelity. A highly specific PCR will generate one and only one amplified DNA fragment of intended sequence from each pair of primers. More efficient amplification will generate more products with fewer PCR cycles. A high-fidelity PCR product has the minimal amount of DNA polymerase-induced errors. Studies have shown the efficacy of PCR is affected by factors including the primer annealing temperature, the activity and concentration of the thermostable DNA polymerase, the PCR buffer components such as dNTPs and MgCl<sub>2</sub>, and the first cycle set-up. Roux, Optimization and Troubleshooting in PCR, *PCR methods Appl.* 4: S185-S194 (1995); Roberston & Walsh-Weller, An Introduction to PCR Primer Design and Optimization of Amplification Reactions, *Methods Mol. Biol.* 98: 121-154 (1998). Special attention has also been paid to the primer parameters, such as homology of primers with their target DNA sequence, primer length, GC content, ratio of primers to the template DNA. Researchers are cautioned that the efficacy of PCR is often a delicate balance among specificity, efficiency and fidelity. Cha & Thilly, Specificity,

Efficiency, and fidelity of PCR, *PCR Methods. Appl.* 3: S18-S19 (1993). Adjusting the conditions for specificity may compromise the efficiency or fidelity and *visé versa*.

The second tier of challenge in multiplex PCR is the presence of multiple pairs of  
5 primers that are unique to multiplex PCR. It is reported that the presence of more than one  
primer pair increases the chance of obtaining spurious amplification products, primarily  
because of the formation of nonspecific DNA extensions, e.g., primer dimers. Markoulatos *et*  
*al*, Multiplex Polymerase Chain Reaction: A Practical Approach, *J. Clin. Lab. Anal.* 16: 47-  
51 (2002). The nonspecific extensions occur when 1) a first primer non-specifically interacts  
10 with a second primer because the first primer shares a certain degree of complementarity in its  
3' sequence with the 3' sequence of the second primer; and 2) when a primer non-specifically  
interacts with a DNA sequence of a template DNA which is not the target DNA sequence.  
Elnifro, *supra*. The nonspecific extensions undermine not only the specificity of PCR but the  
efficiency as well. The nonspecific products compete with desired target DNA, consume the  
15 limited supplies of enzymes, primers and nucleotides, and produce impaired rates of  
annealing and extension. Markoulatos, *supra*. Not surprisingly, the non-specific extension  
limits the number of desired DNA fragments in a single multiplex PCR and poses a major  
limitation to the application and efficacy of multiplex PCR. Lin *et al*, Multiplex Genotype  
Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587  
20 (1996).

So far little progress has been made in combating the nonspecific extension problem.  
Researchers have developed a method to lower the chance of forming the nonspecific  
extension by adding a universal tail sequence to the 5' end of the sequence-specific primers.

Lin *et al, supra*; Brownie et al, The Elimination of Primer-Dimer Accumulation in PCR, *Nucleic Acids Res.* 25: 3235-3241 (1997). The tailed primers are added in a multiplex PCR reaction at very low concentrations and allowed to participate the early cycles of reaction. In subsequent cycles, the primers complementary to the universal tail sequence are added into the reaction at high concentrations and proceeded to continue PCR cycles. This method has reportedly produced 26 DNA fragments and minimized the accumulation of non-specific extensions. Lin *et al, supra*. However, the addition of a tail sequence does not thoroughly tackle the problem of non-specific interaction among primers or between a primer and a target DNA.

Thus, there is a need in the art to design primers that allow the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase chain reaction. There is a need in the art to design primers that minimize or substantially reduce the formation of nonspecific extension of undesired DNA fragments. There is a need in the art to design primers that significantly enhance the efficacy of multiplex polymerase chain reactions.

#### Brief Description of the Drawings

Fig. 1 is an illustration of five forms of primer-primer interactions.

Fig. 2 is an illustration of three forms of interactions between primers and nonspecific target templates.

Fig. 3 is an illustration of a genotyping microarray determining the genotypes of a DNA sample at the 627 loci.

Fig. 4 is an illustration of a set of criteria in designing primers that are experimentally acceptable.

### Summary of the Invention

One aspect of the present invention relates to methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

In one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a first primer and a second primer or the first primer comprises the steps of aligning the first primer and the second primer and selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.
- 5) the maximal match between the first primer and the second primer does not exceed 75%.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a



template DNA comprises the steps of aligning the primer and the template DNA and selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and 2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer;
- 5) the first primer at its 3' end does not contain 15 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary;

6) the primer at its 3' end does not contain 18 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

7) the maximal match between the first primer and the second primer used in the multiplex amplification does not exceed 75%.

Another aspect of the present invention relates to computer products or computer programs which, once executed by a computer process, perform methods as disclosed in the present invention.

The methods according to the present invention increase the number of desired DNA fragments, enhance the efficacy of the multiplex PCR and achieve a significant reduction in cost, time and sample volume. A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments.

The methods according to the present invention significantly broaden the application of multiplex PCR in the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, the gene expression profiling in various samples, and high throughput genotyping technologies which include oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

### Detailed Description of the Invention

The primary aspect of the present invention provides methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

The nonspecific extension of unwanted DNA fragments is a major factor in preventing effective applications of multiplex PCR. The nonspecific extension is caused by nonspecific interactions between different molecules of either the same primer, or different primers, or a primer and a non-primer specific region of DNA templates. Specifically, the nonspecific interactions are caused by 1) a stretch of perfectly matched sequence at the 3' ends of two primers, 2) a stretch of perfectly matched sequence with only one mismatch at the 3' ends of two primers, 3) a stretch of the 3' end sequence of a primer perfectly matching to the internal sequence of the same primer, another primer, or a non-primer specific region of a DNA template, 4) a stretch of the 3' end sequence of a primer perfectly matching with only one mismatch to the internal sequence of itself, another primer, or a non-primer specific region of a DNA template, or 5) a stretch of a sequence in a primer matching to itself, another primer, or a non-primer specific region of a DNA template. Fig. 1. The nonspecific extensions of undesired DNA fragments compete and consume the same reagent components in the PCR reaction and thus impair the production and extension of desired DNA fragments. The problem of nonspecific extensions is aggravated when multiple pairs of primers of high concentrations are present in a single multiplex PCR.

One embodiment of the present invention circumvents the nonspecific extension by setting forth a list of criteria in designing PCR primers useful for multiplex PCR. According

to one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and all the rest of primers including the primer comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer; and
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.

The same method repeatedly applies to the selection of a subsequent primer until all the selected primers meet the above criteria.

According to another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a template DNA comprises the steps of selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

According to another embodiment of the invention, the method of designing primers  
5 to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

5) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;

6) the first primer at its 3' end does not contain seven or more bases that are  
10 perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;

7) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;

8) the first primer at its 3' end does not contain eleven or more bases that are  
15 perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer,

9) the first primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

20 10) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

In practicing the present invention, each primer to be used in a multiplex PCR is selected through the methods described herein. The selection of primers for a large number of DNA templates can be conducted manually or through a computer system. In a preferred embodiment, the methods according to the present invention are conducted through the use of  
5 a computer system.

A computer system according to the present invention refers to a computer or a computer readable medium designed and configured to perform some or all of the methods as described herein. A computer used herein may be any of a variety of types of general-purpose computers such as a personal computer, network server, workstation, or other computer  
10 platform now or later developed. As commonly known in the art, a computer typically contains some or all the following components, for example, a processor, an operating system, a computer memory, an input device, and an output device. A computer may further contain other components such as a cache memory, a data backup unit, and many other devices. It will be understood by those skilled in the relevant art that there are many possible  
15 configurations of the components of a computer.

A processor used herein may include one or more microprocessor(s), field programmable logic arrays(s), or one or more application specific integrated circuit(s). Illustrative processors include, but are not limited to, Intel Corp's Pentium series processors, Sun Microsystems' SPARC processors, Motorola Corp.'s PowerPC processors, MIPS  
20 Technologies Inc.'s MIPs processors, and Xilinx Inc.'s Vertex series of field programmable logic arrays, and other processors that are or will become available.

A operating system used herein comprises machine code that, once executed by a processor, coordinates and executes functions of other components in a computer and

facilitates a processor to execute the functions of various computer programs that may be written in a variety of programming languages. In addition to managing data flow among other components in a computer, an operating system also provides scheduling, input-output control, file and data management, memory management, and communication control and  
5 related services, all in accordance with known techniques. Exemplary operating systems include, for example, a Windows operating system from the Microsoft Corporation, a Unix or Linux-type operating system available from many vendors, any other known or future operating systems, and some combination thereof.

A computer memory used herein may be any of a variety of known or future memory  
10 storage devices. Examples include any commonly available random access memory (RAM), magnetic medium such as a resident hard disk or tape, an optical medium such as a read and write compact disc, or other memory storage devices. A memory storage device may be any of a variety of known or future devices, including a compact disk drive, a tape drive, a removable hard disk drive, or a diskette drive. Such types of memory storage device typically  
15 read from, and/or write to, a computer program storage medium such as, respectively, a compact disk, magnetic tape, removable hard disk, or floppy diskette. Any of these computer program storage media, or others now in use or that may later be developed, may be considered a computer program product. As will be appreciated, these computer program products typically store a computer software program and/or data. Computer software  
20 programs, also called computer control logic, typically are stored in system memory and/or the program storage device used in conjunction with memory storage device.

In one embodiment, a computer program product as described herein comprising a computer memory having a computer software program stored therein, wherein the computer

software program when executed by a processor or in a computer performs methods according to the present invention.

An input device used herein may include any of a variety of known devices for accepting and processing information from a user, whether a human or a machine, whether local or remote. Such input devices include, for example, modem cards, network interface cards, sound cards, keyboards, or other types of controllers for any of a variety of known input function. An output device may include controllers for any of a variety of known devices for presenting information to a user, whether a human or a machine, whether local or remote. Such output devices include, for example, modem cards, network interface cards, sound cards, display devices (for example, monitors or printers), or other types of controllers for any of a variety of known output function. If a display device provides visual information, this information typically may be logically and/or physically organized as an array of picture elements, sometimes referred to as pixels.

As will be evident to those skilled in the relevant art, a computer software program of the present invention can be executed by being loaded into a system memory and/or a memory storage device through one of the above input devices. On the other hand, all or portions of the software program may also reside in a read-only memory or similar type of memory storage device, such devices not requiring that the software program first be loaded through input devices. It will be understood by those skilled in the relevant art that the software program or portions of it may be loaded by a processor in a known manner into a system memory or a cache memory or both, as advantageous for execution.

As will be appreciated by those skilled in the art, a computer program product of the present invention, or a computer software program of the present invention, may be stored on



and/or executed in a PCR instrument. For example, a computer software of the present invention can be installed in, for example, the Smart Cycler System, the Idaho Rapid Cycler, the Carbett Roter-Gene System, the GeneAmp 5700 Sequence Detection System, the ABI Prism7000, 7700 & 7900 Sequence Detection Systems, the iCycler System, the MX-4000  
5 Multiplex Quantitative PCR System, the DNA Engine Opticon System, the Perkin-Elmer 9600 cycler, and MJ Research's DNA Engine Opticon System.

However, it is not necessary that the computer program product or the computer software program be stored on and/or executed in a PCR instrument. Rather, the computer product or software may be stored in a separate computer or a computer server which may or  
10 may not connect to the PCR instrument through a data cable, a wireless connection, or a network system. As commonly known in the art, network systems comprise hardware and software to electronically communicate among computers or devices. Examples of network systems may include arrangement over any media including Internet, Ethernet 10/1000, IEEE 802.11x, IEEE 1394, xDSL, Bluetooth, 3G, or any other ANSI approved standard.

15 In a preferred embodiment, a computer program termed MULTIPLEX is developed to select primers according to the methods as described in the present invention. See Table I for the flowchart of MULTIPLEX program.

Even with the assistance of MULTIPLEX, it is time consuming to analyze exhaustively all possible sequences frames and select the best possible frames for PCR  
20 primers. To expedite the computer-assisted selection process, a strategy termed "random fitting" is developed. Under the random fitting strategy, a set of criteria for the length of the matching sequences is set forth for primer selection. See Table I.. For example, when the number of 3' end matching bases is less than 4, the experimental effect of this

complementarity is neglected. Therefore, the criterion for the length of 3' end complementarity was set to be less than four. With the predefined criteria, the MULTIPLEX computer program first randomly picks up a pair of primers for each target sequence. All possible interacting pairs in this combination are examined. Record is made on qualified and unqualified primers in the combination. The program then randomly picks up a new pair of primers for each target sequence that collectively form a second combination. If the number of qualified primers in the second combination is less than that in the first combination, no record is made. The MULTIPLEX program, however, begins to examine a third combination. If the number of qualified primers in the third combination is greater than that in the first combination, the first primer combination is replaced by the third one in record. The program keeps processing until a combination with all qualified primers is found. Under the random fitting strategy, the MULTIPLEX program can select qualified primers for 100 sequences within two hours, 500 within two days and 1,000 within two weeks. The "qualified primers" are those primers fully conforming with the selection criteria set forth in the method of the present invention.

To further improve the MULTIPLEX program, another primer selection method called linear primer selection is also used as an alternative. See Table I. With this strategy, instead of selecting the frames randomly, each frame of a pair is selected from one end of the defined range of a sequence. The selected frame pair is then examined. If these frames are qualified as primer sequences, the selection of primers for the corresponding sequence is completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences. The newly selected frames are then examined. If these frames are qualified as primer sequences, the selection of primers for the corresponding

sequence is then completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences... If the frames are slid to the other ends but not qualified frames are found, the lengths of the frames will be increased by 1 base. The same process described above will be repeated. The sliding and length changing process repeats until a pair of qualified frames is found. If no qualified frames can be found after exhausting all possible frames for a sequence, the sequence will be labeled as unusable, and will be excluded from the multiplex set. This method is called linear primer selection.

When the number of sequences is large, the random primer selection method may be used for selecting primers of only a fraction of sequences. The random selection process is stopped at a point defined by the user. The program can then switch to linear primer selection method. We have shown that appropriate combination of these two methods can increase the selection speed by several tens to >100 fold compared with using the random method only.

It needs to be pointed out that the MULTIPLEX method can be used not only for primer selection of SNPs, but also for primer selection of any other DNA and RNA sequences if a position is defined so that it can be used to separate a sequence into two parts for selecting the two primers, respectively.

Following the selecting and synthesizing of qualified primers, DNA templates are contacted with multiple primers for the amplification of desired DNA fragments under conditions suitable for multiplex PCR developed in the inventor's laboratory. These conditions are: 2.0 mM MgCl<sub>2</sub>, 50 mM KCl, 100 mM Tris-HCl, pH 8.3, 100 μM deoxynucleotide triphosphates (dNTPs), and 10 units/50 μl "HotStart" *Taq* DNA polymerase (Qiagen, Valencia CA). The PCR mix is first preheated for 15 min at 94°C to activate the DNA polymerase followed by 40 PCR cycles. Each cycle consists of a denaturation step at

94°C for 40 sec, and then an annealing step at 55°C for 2 min followed by a ramping step from 55°C to 70°C within 5 min. After the PCR cycles, the samples are incubated at 72°C for 3 min.

A DNA template to be used in practicing the present invention includes without  
5 limitation eukaryotic, prokaryotic and viral DNA. The DNA may be obtained from any cell source or body fluid. Non-limiting examples of cell sources available in clinical practice include blood cells, buccal cells, cervicovaginal cells, epithelial cells from urine, fetal cells, or any cells present in tissue obtained by biopsy. Body fluids include blood, urine, cerebrospinal fluid, semen and tissue exudates at the site of infection or inflammation. DNA  
10 is extracted from the cell source or body fluid using any of the numerous methods that is standard in the art. It will be understood that the particular method used to extract DNA will depend on the nature of the source. The preferred amount of DNA to be extracted for use in the present invention is at least 5 pg which is corresponding to about 1 human cell equivalent of a genome size of  $4 \times 10^9$  base pairs.

15 A primer designed in accordance to the method in the present invention is from 17 to 50 nucleotides in length, preferably 20 to 35 nucleotides in length. The concentration of a primer in the multiplex PCR reaction can range from 0.1nM to about 4μM per reaction, preferably from 1nM to 0.1 4μM per reaction.

Multiplex PCR reactions are carried out using manual or automatic thermal cycling.  
20 Any commercially available thermal cycler may be used, such as, e.g., a Perkin-Elmer 9600 cycler.

The resultant multiple amplified DNA fragments of interest are analyzed using any of several methods that are well-known in the art. For example, agarose or polyacrylamide gel

electrophoresis is used to rapidly resolve and identify each of the amplified sequences. When a gel is used, different amplified sequences are preferably of distinct sizes and thus can be resolved in a single gel. The reaction mixture can further be treated with one or more restriction endonucleases prior to electrophoresis. Alternative methods of product analysis include without limitation dot-blot hybridization with allele-specific oligonucleotides, single-strand conformational polymorphism analysis, high-throughput genotyping platforms including oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

The multiple primers designed in accordance to the method in the present invention minimize the nonspecific interaction between primers or between a primer and nonspecific target sequence of a template DNA. Accordingly, the use of these primers in a multiplex PCR minimizes the formation of non-specific extension of undesired DNA fragments and maximizes the specific interaction and amplification of desired DNA fragments.

Furthermore, the method in the present invention increases the number of desired DNA fragments, enhances the efficacy of the multiplex PCR and achieves a significant reduction in cost, time and sample volume. Finally, the multiple primers designed in accordance with the methods of the present invention may be used in real time PCR or multiplex real time PCR.

A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments. It is preferred that the single multiplex PCR contain at least 100 pairs of primers and produce at least 100 desired DNA fragments.

The present invention significantly broadens the application of multiplex PCR in the art which has been limited by the nonspecific extensions of unwanted DNA fragment and the number of desired DNA fragments it could produce. Given a large number of multiple desired DNA fragments that a multiplex PCR now can produce using primers designed under the present invention, the multiplex PCR can now be fully used in applications including but not limited to the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations in cancers, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, and the gene expression profiling in various samples.

The following examples are intended to further illustrate the present invention without limiting the invention thereof.

EXAMPLE 1. Selection of 627 pairs of primers.

648 single nucleotide polymorphism (SNP) markers were initially selected from the SNP Database maintained by the National Center for Biotechnology Information. To facilitate the genotyping after PCR, all these SNPs were transition polymorphisms that were A to G or C to T changes at their polymorphic sites. All SNP sequences were analyzed by the computer program MULTIPLEX to determine whether these SNP sequences are unique in the genome. The repetitive sequences were discarded. PCR primers were selected by using the computer program MULTIPLEX described above with the following values:  $T_m$  range = 75-104°C, primer length range = 24-33 bases, 3' perfect matches <4, 3' match with 1 mismatch <7, 3' end matching internal sequences of other molecules <9; 3' end matches internal sequences of other molecules with 1 mismatch <11; maximal match between different molecules, 75%). The quality of each pair of primers was examined individually by using them to amplify their

target sequences. Only the primer pairs with high specificity and yield, as judged by gel electrophoresis, were used for multiplex amplification. At the end, a panel of 627 SNPs was selected from the initial 648 SNPs as shown in Table II and Table III. Table II is an illustration of a list of 627 single nucleotide polymorphism (SNP) markers selected from 648 SNP markers. Table 3 is an illustration of a list of 627 pairs of primers and probes that were designed according to the method disclosed in the embodiment of the invention, used in a single multiplex PCR reaction, and used for genotype determination by analyzing the multiplex PCR products by microarray.

EXAMPLE 2. Using 622 pairs of selected primers in a single multiplex PCR.

For the multiplex PCR, lysate for 500 cells from a tissue cultured cell line, MG2314, was prepared. The reason for using cells instead of purified DNA is that they could be precisely quantified and equal number of nearly equal number of copies of the target sequences could be used as the starting material. PCR mix contained 1 X PCR buffer (100 mM Tris-HCl pH 8.3, 150 mM KCl, 1.5 mM MgCl<sub>2</sub>, and Gelatin 100 µg/ml), primers (10 nM each) for all SNPs, the four dNTPs (100 µM each), Taq DNA polymerase (5 units) with a final volume of 30 µl. Sample was preheated for 15 min at 95°C. Each PCR cycle consisted of a denaturation step at 95°C for 40 sec; annealing at 55°C for 3 min; and a step for both annealing and extension with temperature ramping from 55°C to 70°C within 5 min. A 3 min incubation at 95 °C as added after the PCR cycle to minimize the incompletely extended PCR products. PCR was completed after 40 cycles.

EXAMPLE 3. Analysis of multiple DNA fragments after the multiplex PCR

To resolve the allelic products in the multiplex PCR product for genotype determination, single base extension and microarray methods were used. Two

oligonucleotides with completely complementary sequences for each SNP were synthesized for this purpose. One of these was called E probe that was using in the single base extension assay. The other was called A probe that was spotted onto a coated glass slide. E probes had sequences with their 3'-ends next to their polymorphic sites. In the single base extension  
5 assay, dideoxynucleotides labeled with either the chromaphore Cy 3 or Cy 5 were used. The allelic base at the polymorphic site determined which fluorescently labeled nucleotide could be incorporated into an E probe.

The corresponding A probes were spotted onto a glass slide with a microarrayer manufactured by Cartesian. The fluorescently labeled E probes were hybridized with the A  
10 probes on the microarray. The signal intensity for the alleles of each SNP was determined by using the computer software for image analysis from Biodiscovery. See, Fig. 3.

To validate the results from microarray analysis, the genotypes of the cell line used in the study were determined for all 622 SNPs by restriction enzyme digestion method described by Li & Hood, Multiplex Genotype Determination at A DNA Sequence Polymorphism  
15 Cluster in The Human Immunoglobulin Heavy-Chain Region, *Genomics* 26: 199-206 (1995). A few SNPs that could not be analyzed by this method were analyzed by direct sequence analysis.

Because all SNP were transition polymorphisms, all E probes could be analyzed by either A and G or T and C. In either case, consistent results from 85% (for labeling with A  
20 and G) to 90% (for labeling with T and C) SNPs were obtained by both microarray and the restriction digestion methods. A probes for A and G labeling were used for 85% of SNPs, and others were replaced by those for T and C labeling. Fig. 5.



Papers and patents listed in the disclosure are expressly incorporated by reference in their entirety. It is to be understood that the description, specific examples, and figures, while indicating preferred embodiments, are given by way of illustration and exemplification and are not intended to limit the scope of the present invention. Various changes and  
5 modifications within the present invention will become apparent to the skilled artisan from the disclosure contained herein. Therefore, the spirit and scope of the appended claims should not be limited to the description of the preferred versions contained herein.

## Flow Chart - General

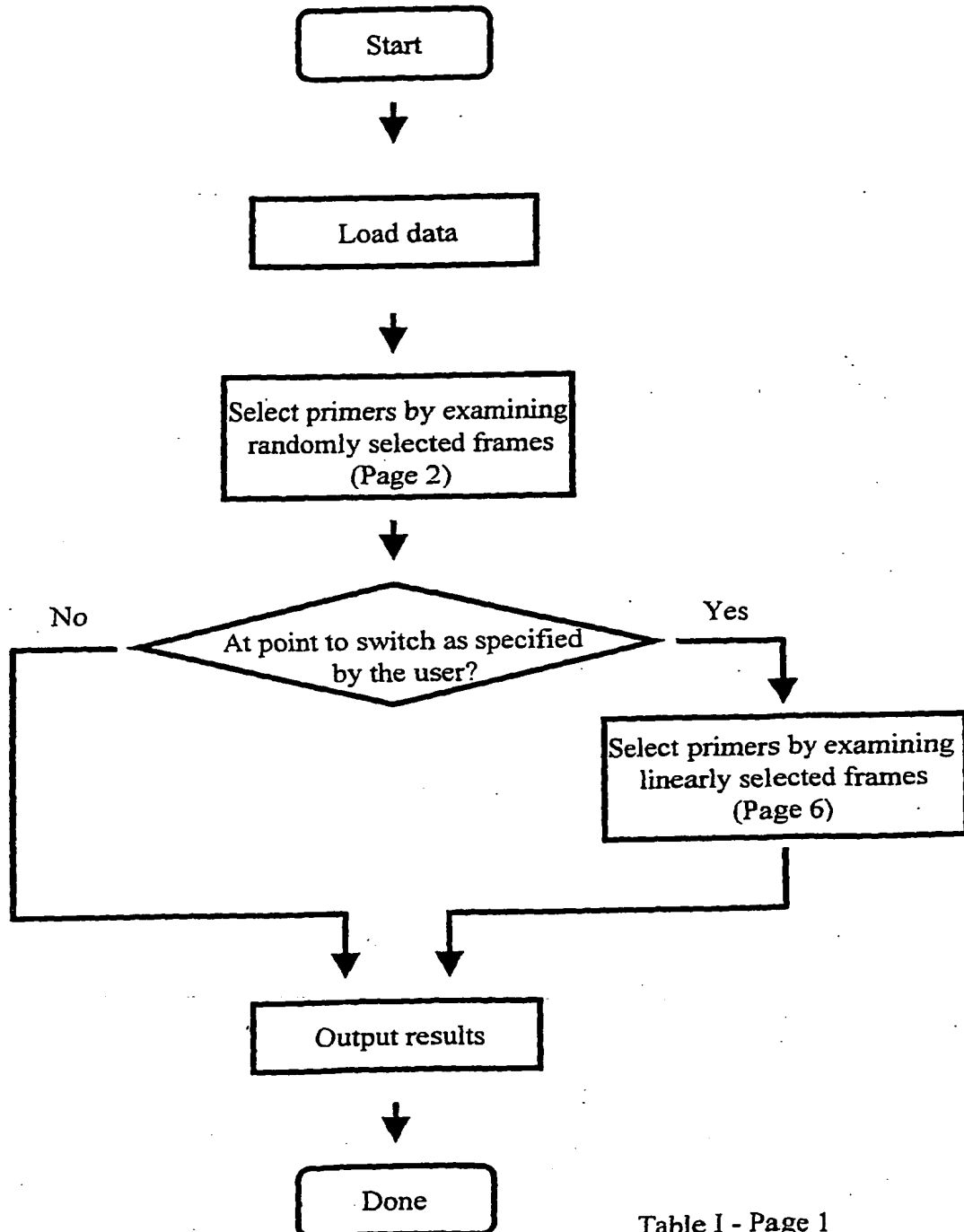


Table I - Page 1

## Page 2 – Select Primers by Examining Randomly Selected Frames

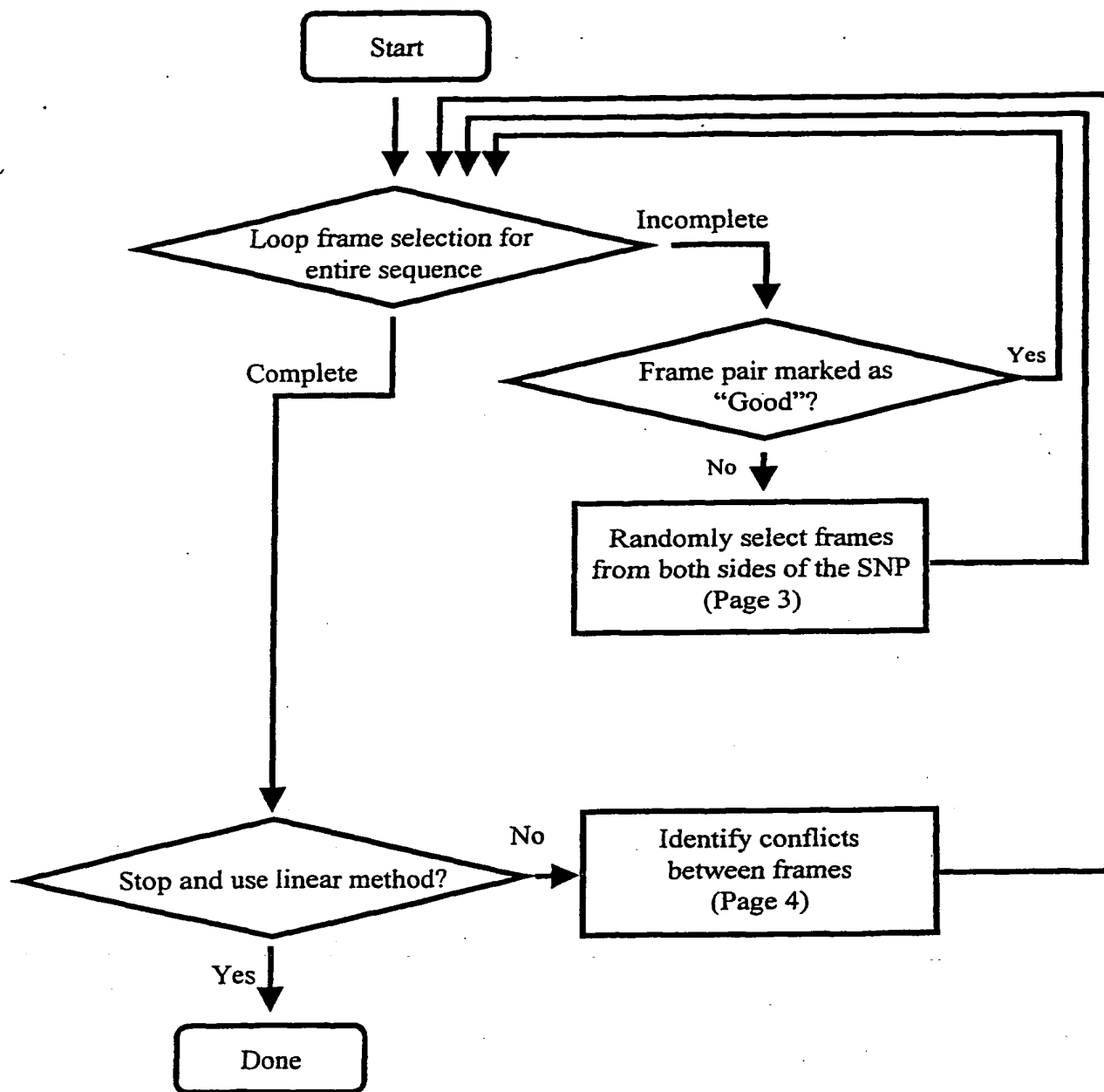


Table I - Page 2

### Page 3 - Randomly Select Frames from Both Sides of Each SNP

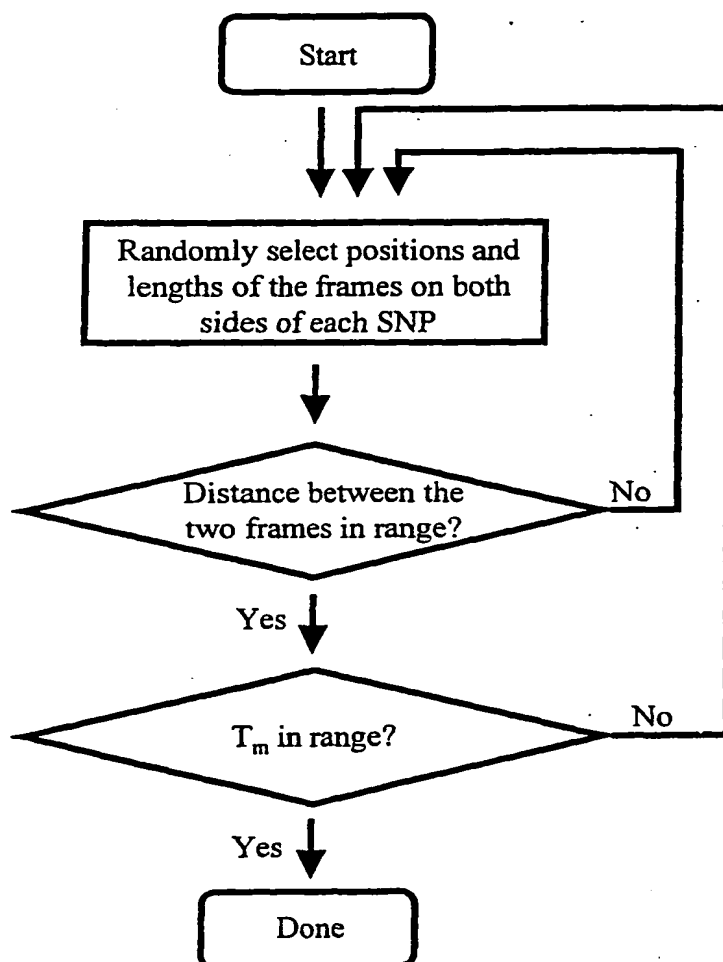


Table I - Page 3

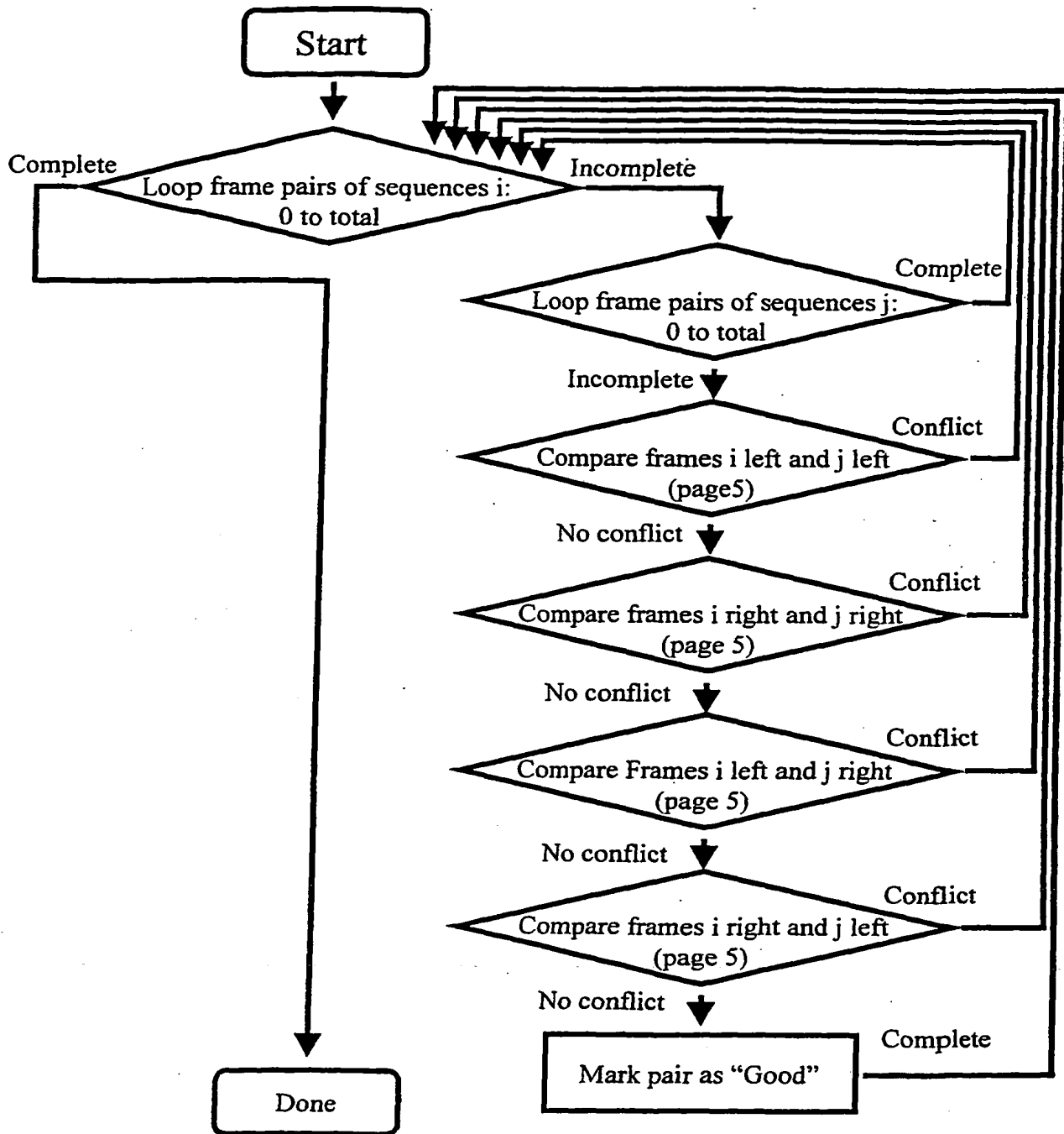
**Page 4 - Identify Conflicts between Frames**

Table I - Page 4

## Page 5 – Compare Selected Frames

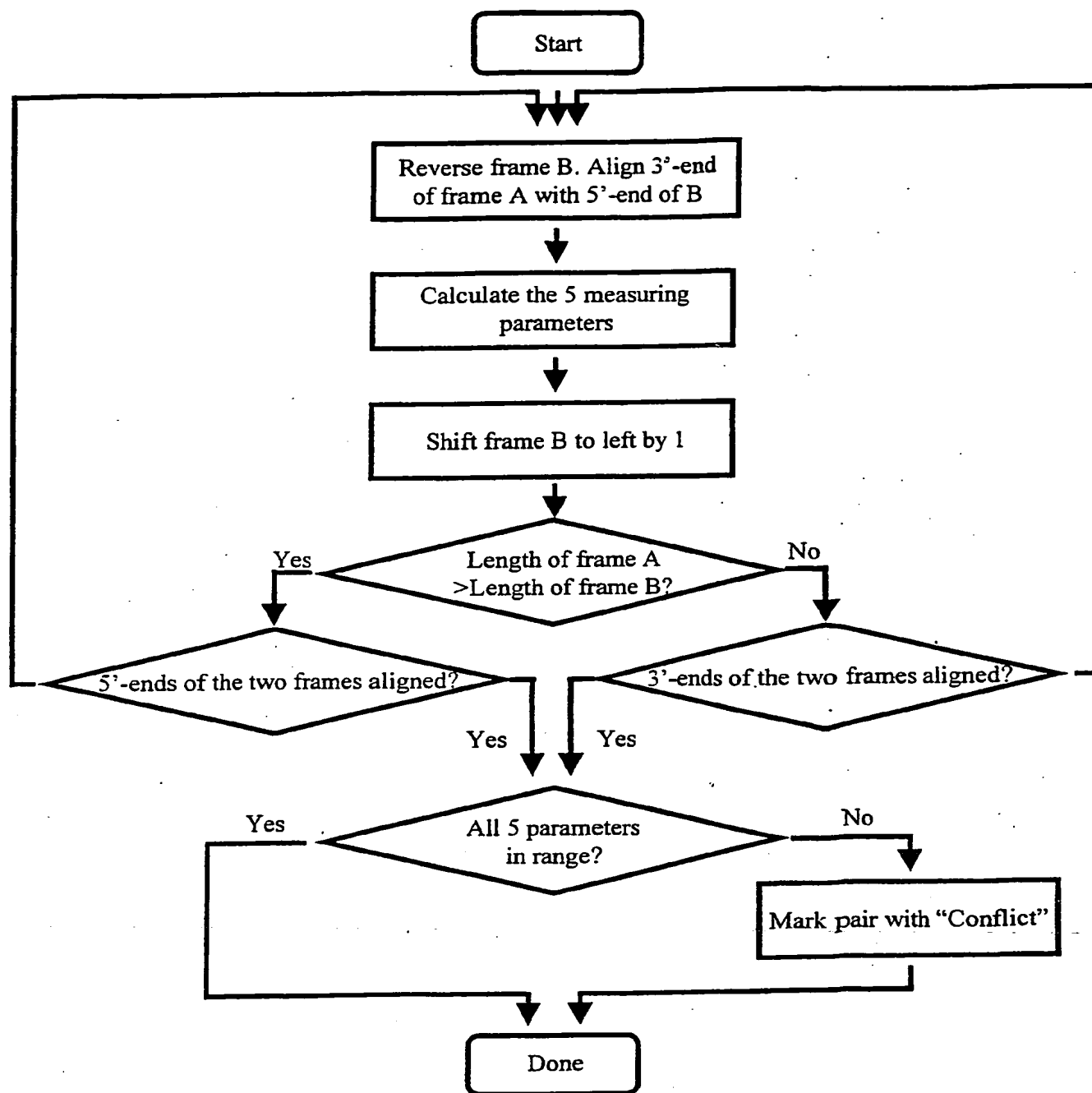


Table I - Page 5

## Page 6 - Select Primers by Examining Linearly Selected Frames

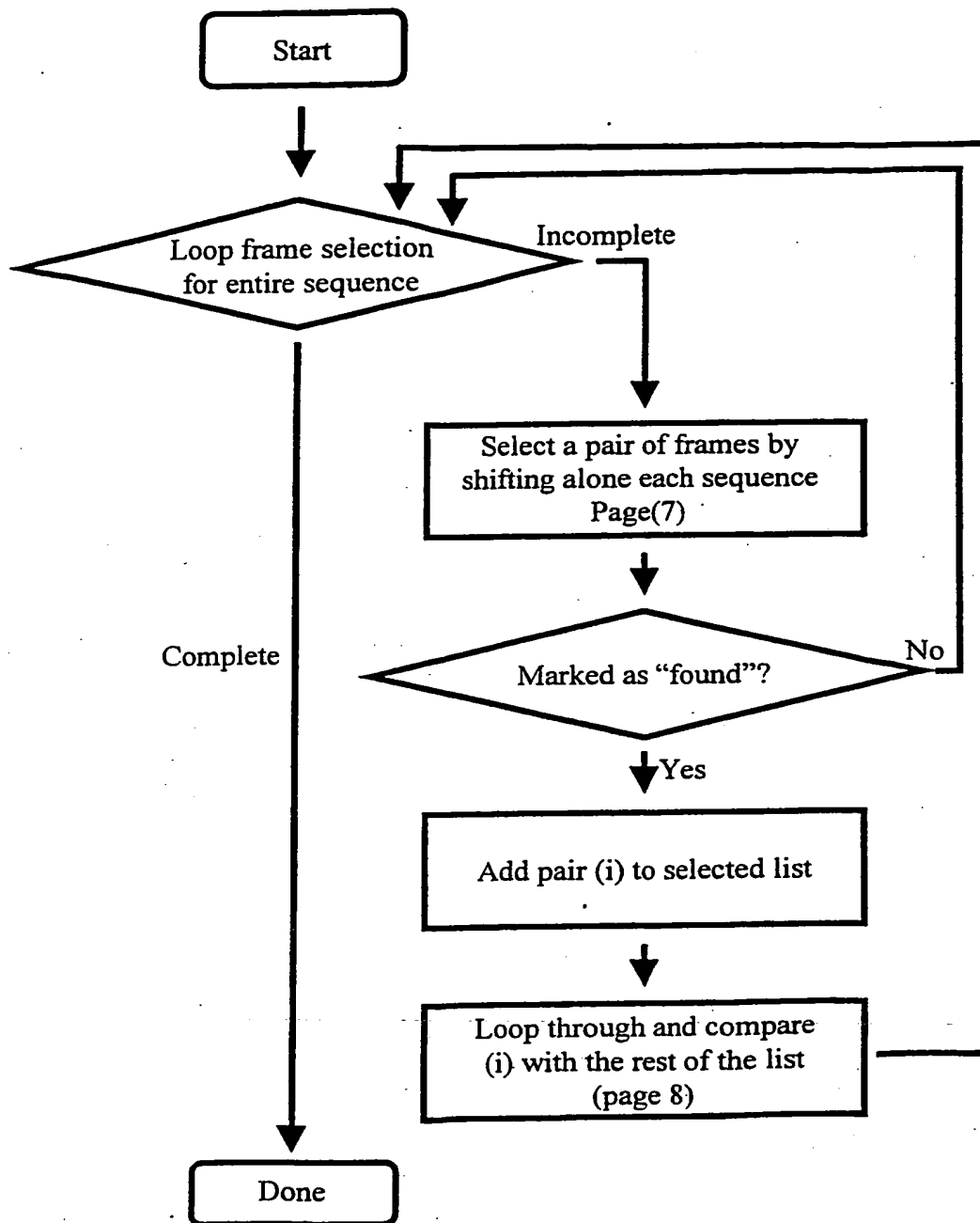
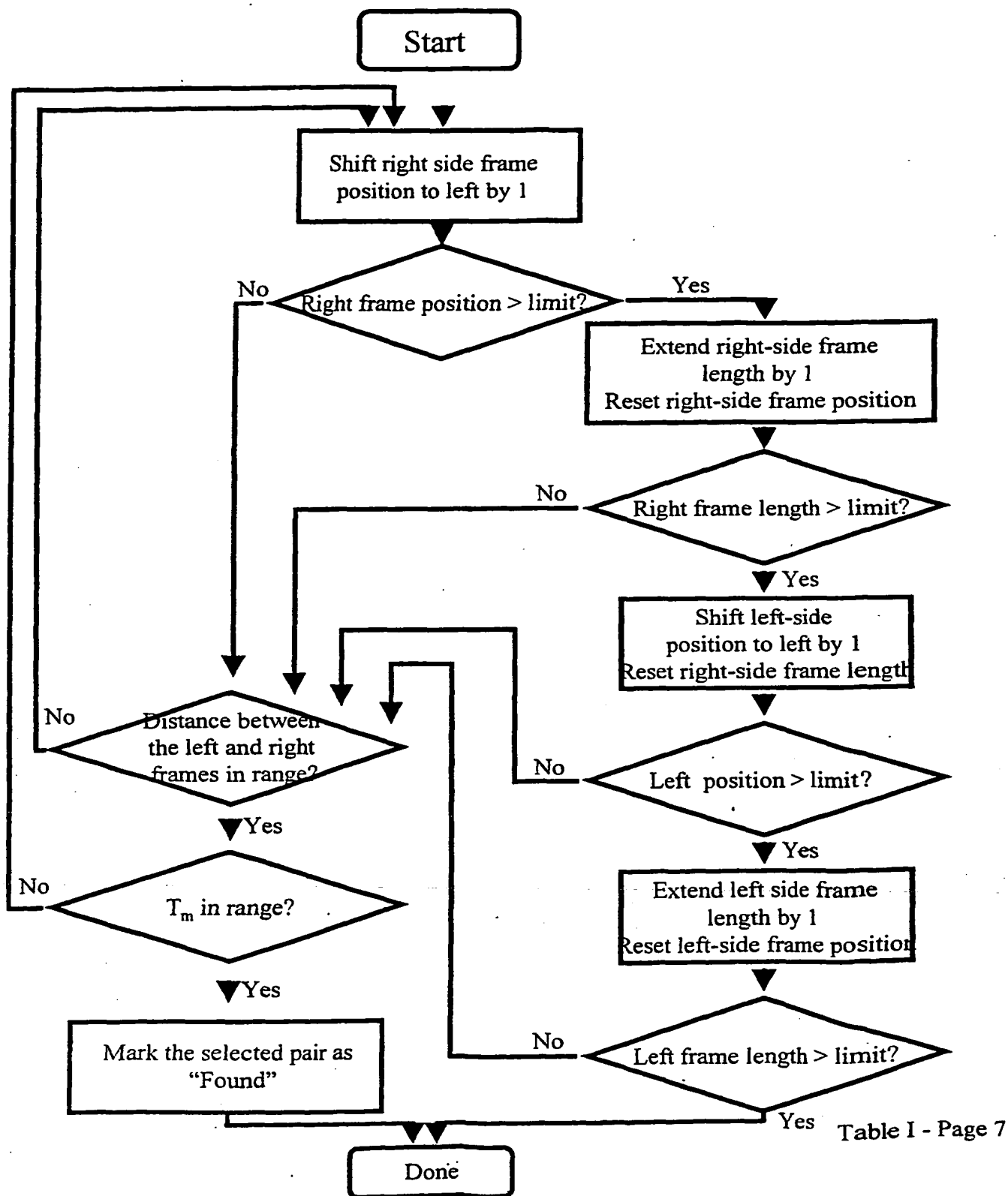


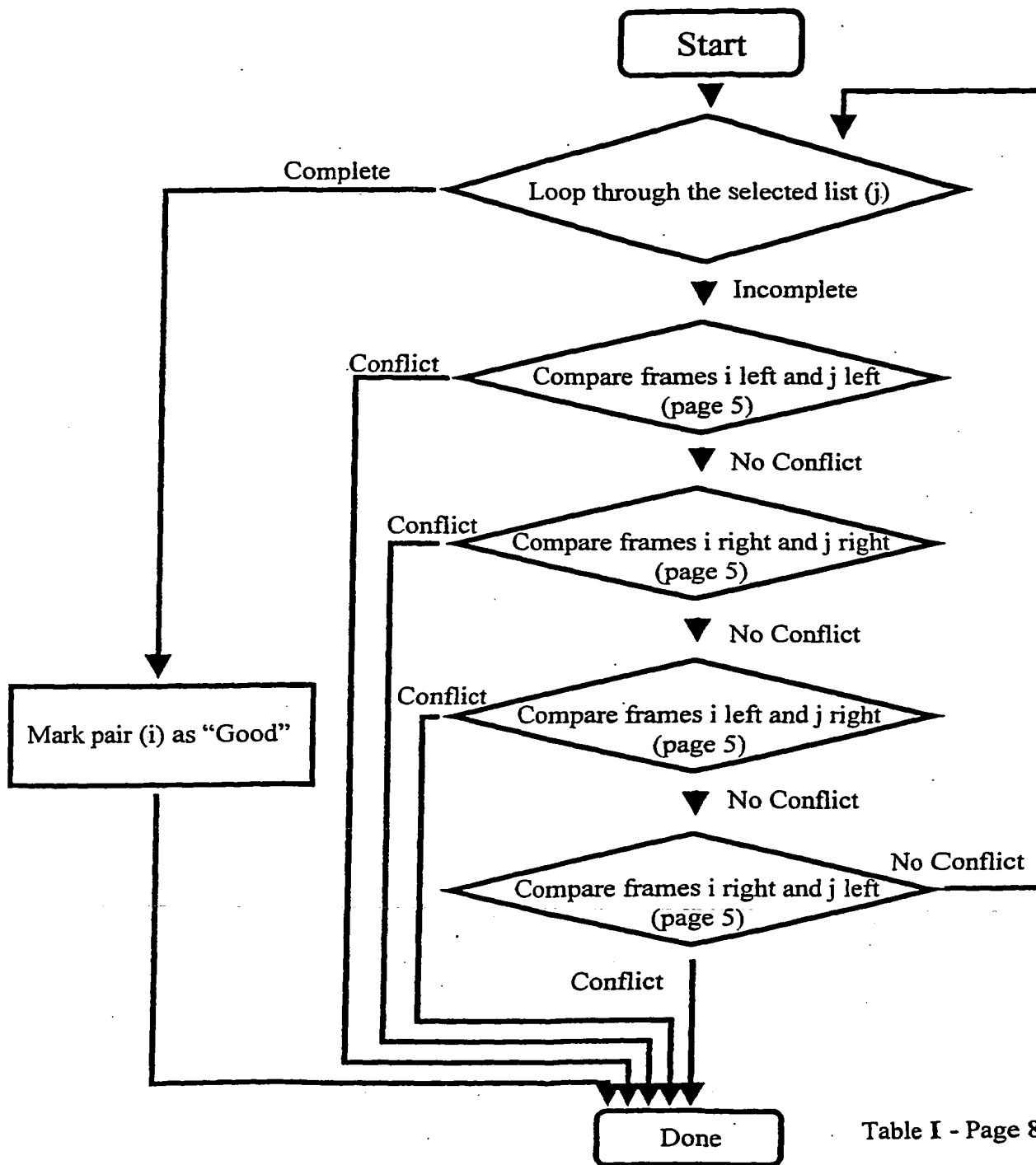
Table I - Page 6

# Page 7 – Select a pair of frames by shifting along each sequence





# Page 8 - Loop through and Compare Frames i with the Rest of the List





SNP		Left Primer		Left Primer		Right Primer		Right Primer	
Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')
01T091L	ATTTGGAGCCATAAACAATATCTAA	01T091R	TGTGTGTTTAACTGTGCAAGTAT	01T091E	CATAATAATGTTATGCTCTGGCCACA	01T091A	TGTGGCCAGAGAGTAAACATTTATATG	01T090E	CTTCTCTGACCCACACAATTTAAATTTGTA
01T094L	TGCAATCTCCGCCAAAGTGA	01T094R	TACCTTGCTATGACACAGATTAT	01T094E	GCAACATGGGCTATAGGAGAGATCC	01T094A	GGATCTCTCTATAGCCCATTTGTC	01T090A	TTACAATTTTAAATTTGTGTGTCGACGAAGG
01T096L	TCAGTGCCAGAAAGATTTGGCTTA	01T096R	TGGTCTCTATGAGCATCTAGT	01T096E	GTCCTCTTAATGTGGAGCTAGACACT	01T096A	GTGCTGAGCTCCACATTAAGGAGATCG		
01T097L	CAGGCTCTCTTCTGTGAGAGCGCC	01T097R	AAGTCCTACAGGCATATAT	01T097E	GTTCTGGTCTCTGTGGGCTCCGC	01T097A	GCGGGACCAAGGACACAGAAC		
01T098L	GGCCAAAGTATATACACTGTGTAG	01T098R	ACTGAGGCCAGAGAGGGGATGAC	01T098E	GTACGGCTGGAACTGTGGAAACCCAA	01T098A	TTTGGGTCCAGTTCCAGCCGTAC		
01T099L	CCATATGCTGTCTCAGGGCAT	01T099R	TGTTAATATCTTCCAGCCATCAG	01T099E	TGCCCTGCACATACTACTCTGTGGCT	01T099A	AGGCCAGGAGTAGTATGTGAGGCA		
01T101L	AGAAGCCAGTGTCCAGAGGAT	01T101R	CTCCCATCACTACTCTCCACCT	01T101E	CCTTAGGCCACCCGTGTGCTGCTTA	01T101A	TAAAGCAGACACAGGTTGGCTTAGG		
01T103L	CACAGGGTGATCAGGACAGCTT	01T103R	ATCTGGCTCTCTCTGGAGATGT	01T103E	CTCTCTAATAAGAGGTATGCAATTAATGC	01T103A	GCATTAATTCATCTACTCTCTTATAGAGC		
01T104L	CTGGGAAGACGTCTCTTCAA	01T104R	ACACTAATACAGAAAGTCTGTATA	01T104E	GAGGATTTGCTGTTAGGTATTTATCTC	01T104A	GAGATAAATATCAACAAAGCAATCTC		
01T105L	AAATGCTGCAGCTCGCCCT	01T105R	GAQGCCACAGCTCAGAGATC	01T105E	CTCTGTGCTCTTGTGCTCAACAAAC	01T105A	GTTTGTGTGGCATCAACAGGAGACAG		
01T108L	GGATGAGAAGGAACAAGCCGTGT	01T108R	TTCATCTGTCTAGTTTCTGCC	01T108E	GGTGAAATGGAAATGTCACGAAAGCCCT	01T108A	AGAGGCTTTCTGCACATCTCATCTTACC		
01T109L	CATTGTGTGCTGTCTCTCTC	01T109R	TGGAATGCGTATGAACCTTAC	01T109E	CAAGCTACATCTCGAAGGCTGTGATCC	01T109A	GATCAAGAGCTTCGACATAGTAGCTCG		
01T111L	GGCTAATTGGAATGGTAA	01T111R	ATACATATTTTCTCAATGTGTGA	01T111E	GTGTGAAGAGTAATAATACTTTAAGATGG	01T111A	CCATCTTAAATGTATTATTACTCTTCAAC		
01T117L	CTCTCATCTCTCTAAAGGAAAA	01T117R	CTTTTATTTGAATCTTTTGACAG	01T117E	GCACATGATTTATTAATAAGCTTTTTC	01T117A	GGAAAGGCTAATTAATAAATAATCATGTGC		
01T118L	TGCCAATCTCTTGGCAAAATCAA	01T118R	TTTATGTGGAGATGTGTGCTA	01T118E	ATAGCTCTCAAAACAGGGAGACAG	01T118A	CTGCTCCCTGGGTGGAGACGATT		
01T119L	GCCAGGGCTGATGGCAGTGAAAC	01T119R	TCCCTTTAATCTCCACACT	01T119E	GCAGTGAACAAACAGATGATATAGCTTAC	01T119A	GTAAGCTATAACTCATCTGTTTGTTCATGC		
01T120L	CTCTAATATCCCAATCTTTGG	01T120R	TACAGAGGCTGCTCCACACTTGG	01T120E	GGGCAATATACAGAACGACTTTC	01T120A	GAAATGGGCTTGTGTATATATCCCC		
01T121L	GAGCAGGGTAAAGCAGGATCA	01T121R	GGCCAGTATCTCCGCTCTTA	01T121E	CTCAGGGCTGGCTGTCTTAACTGCTC	01T121A	GAAAGGCTTAAAGCAGACGCTGAG		
01T127L	GGAGCTGCCCAGAAACAGCCCTG	01T127R	CTGATCTGCACACAGGATCAG	01T127E	TGGGTGGGCTTGTGTCTGTAGTCT	01T127A	AGGTACAGACACAAACCCCAACCCA		
01T128L	TCCCAGGGCTCTGTGGCTCTG	01T128R	GTCCAGAGGACGAGGCCCTG	01T128E	CATGTGAGGAGCAGAGCTCCCATC	01T128A	GATGGAGGCTCTGGCTCTCTCATATG		
01T129L	ACCCAATATGCCAGTTAATACTGAC	01T129R	GGGAGTGTGTCTACCAAGCTTAA	01T129E	CCAGACTCTTCCCACTAAACTGTTTC	01T129A	GACAATCTGTGATGGGAAAGTGTCTGG		
01T131L	CCCTGTTATTTCCAGAAATACTAG	01T131R	CTCTTCCAGAGCACTAGGGTA	01T131E	CTCAAGCTGTACTACAGAACCACTAA	01T131A	TACTGGGTGAGTAAACAGCTGACTG		
01T133L	CTATACAAATATGACAAGAAGGCG	01T133R	TTTCTTGAAGTCTGTGTGTCAT	01T133E	TAAACAGCTTTTACACAGAAACAACAA	01T133A	TGTTGTTTTTTTCTTTAAATTTTGTAA		
01T135L	TAAAGTCTTTATGCTTCTCCACC	01T135R	AGGAATAGGATATGGTTTCTTG	01T135E	GTCACTCAGCCTTACACAGAAATAATCTGATA	01T135A	TACAGATTTTCTTTAAATGGCTGAGTAC		
01T137L	AAAGAGAAACACCACTCTTA	01T137R	ATTGGAAATCCCTTACTCTGTATA	01T137E	CTCTCCCTCTGAGAGGGCTGGTGA	01T137A	TACCAAGGCTCTCTCAGCGGGAG		
01T138L	GAAATGATATCAACCAACTTC	01T138R	ATTATCCCACTCTCAGGTAGTATC	01T138E	GAGATGGAGCTAATCAACAGCCCTC	01T138A	GAGGCTTGTGTATGATGCTCATCTC		
01T143L	GGCAGCTGGAGGTTAAGCATCTAA	01T143R	CAGGAGAGCTGGATGATCTCGA	01T143E	CCTGAACACCAACATAGAAGGCCAC	01T143A	GTGGCTTCTGATGTGTGTGTCTAGG		
01T146L	ATTGTTAGTCTCCCACTTTGA	01T146R	TGGTGAATGAATCATGTCTCTCGC	01T146E	CAGACACATGGAGCTAGCTGGAGA	01T146A	TCCGAGCTAGCTCCAATGTGCTGCTC		
01T147L	AATGATAGAAGCTAGTGTAAAC	01T147R	TGTGGCATGTATAACTAATGACT	01T147E	CATTACTGATGTATCTCAAGTCTTGCCA	01T147A	TGGCAAGCTGAGAGATCATCTAGTAATG		
01T148L	AGGAAGATATAGAGAAACTCTA	01T148R	TCTTGATATGCGCAGCTGTGACAC	01T148E	GAGTAAATCAATGGCTCATGGAGTCT	01T148A	GACTCCAATGAGCATTAATTAATCTTC		
01T150L	TCAGAAGATCTGTTGAACCTCTGG	01T150R	TTTATTGAGTCACTCTCTCTCTG	01T150E	TGTTGCCAGGCCACAGAGTGAATGG	01T150A	CCATTACACTCTGGCTGGGCCAACA		
01T151L	GCAGTTGGCCCTTTTATC	01T151R	CCCAAGAGGCCACAGAGGAAA	01T151E	CCCTGTGTGTGTGACAGCTAAGGA	01T151A	TCCCTAGGCTGGCAACACAGAGG		
01T152L	TTCTTAAGCTTCAATCTGGCTTG	01T152R	ACCAATTTTAAACTCCCTTTGGA	01T152E	AGAAAGGCTTTGGAAGGCTACCTG	01T152A	TCCGTAGCTTTTCAAAAGCATTTTCT		
01T153L	ACTGGATATGCTCCAGGTAT	01T153R	GAGTGCACAGCAAGATTAAT	01T153E	TTTATATGGCCCTTTTATGCTATATAACATA	01T153A	TATGTTTATATAGCATAAAGGGCAATATAA		
01T154L	CCATCTCCCTCTAAAATA	01T154R	TCTCTTAGGTCAGTGTCTTA	01T154E	GAAATAATGATGTTTTCACACATAAATTCG	01T154A	TTGTAATAGCAGATATAACATATTATTC		
01T155L	GGAACCTCTGATGAATACTAAAC	01T155R	AGCGGAATGGATGAATCTG	01T155E	CTGAGTATCCAATTTCTCTGCTATTCAA	01T155A	TGTAATAGCAGATATAAGGAATGGATCTCAG		
01T156L	TCCTCTCCCTGGTGTGGGGCTT	01T156R	GAGCAATCATTTTGAACAACT	01T156E	ACTGGGCTGATGATATATGATGG	01T156A	CCAATCAATCATCATAAGCCCATC		
01T157L	AGCATGTCGGATTTTCATGACT	01T157R	TATACAGTGTAGTATAGAGAGGC	01T157E	GAAATGATGATGTTTGAAGGAGACATTC	01T157A	TGDTCTCTCTTCTACTCATCATCTC		
01T159L	GTGAGTCAATTTGGCCTCTTGA	01T159R	GTGAGCTCTGAGAGCTTT	01T159E	CTCTAGCTTAATTTGGGCATTTAAAGTT	01T159A	AACCTTAATAATGCCACAATTTACGTAGG		
01T160L	CCCTATGTCCCAACAACCT	01T160R	ATATATTTTGAAGGCCAACAG	01T160E	AGATCAAAATATTATTAACCTGATAACTAAMAA	01T160A	TTTATGTTATTCAGGTTAAATATTCTTGATCT		
01T162L	AATTAGGTTTGAAAGGGGAAATAG	01T162R	TCAATAAATAATCTCTTGCCA	01T162E	GAAACAAATATAGTCTGTATAGTAACTATGCT	01T162A	AGCATAGTACTATACAGACATAATTTGTTTCT		
01T164L	TAAAGTTTGTCAGAAAGGATTC	01T164R	TGAAGGAAGGCTCTGAGGCAT	01T164E	GGCAGCTACAGGTGCACAGACTCTCAGA	01T164A	CTGAAAGCTGTGACCTATGACATGACCTC		
01T166L	CACATTCTTTTCCATGTGTAT	01T166R	TCCAACACATAGTAATTTTCCA	01T166E	ATATATATGACTCCCTCTTAAATGCC	01T166A	GCGATTTTGAAGAGGAGGTCTATAATAAT		
01T167L	ACAAAATTTTAAATGCTGTGGA	01T167R	TTTACAGTCTCCAAAGGACTCAG	01T167E	CCCGCTTAAATTTTATGTTTATG	01T167A	CATAAAACCTATAACATAAAGCCGG		
01T169L	ACAAAATCTTCCCAAGACTCA	01T169R	TTTACGCTTAATCACTGTGCTC	01T169E	GGAGATCAAAATCTCTCTACGACATAACA	01T169A	TGTTATGTGCTAGTAGGAATTTGATCTTC		
01T171L	GCAAAGGGTAAGAGAGGAAAGTGGC	01T171R	CTGGGTTCCACATCTCTCCAGTTAT	01T171E	AGAGCTGTTTCCACTATGGGCTT	01T171A	CAGCCCATAGGTGAAACAGACTTCT		
01T172L	ACATCAGGGCTGTACTCTGTGG	01T172R	TTTGTGCTTAATCACTGTGCTC	01T172E	TTTACGCTTAATCTGTTTATGTTATG	01T172A	CCCATCTGCTCTTGTCTCAAGTCCA		
01T173L	TATAGAAAGATCCCATAGCAATG	01T173R	TTTACTGTGTGGACAAAT	01T173E	CACAAATATAGAAACTTCTTGGCTGA	01T173A	TACGCCAAAGCAAGTCTCTAATTTGTG		
01T174L	AGACGTTCACTGATATCTCTCC	01T174R	AATTAAGCCACTTGAATA	01T174E	GAGTACTGATAAGGAGGCTCTCAAG	01T174A	CTTATGAAGCTCTCTCTTCAAGTACTC		
01T176L	CAGCTGAGGCATTAATATTCAT	01T176R	AGTGAAGATACCCAGTACCTCAGT	01T176E	TTGGGGGGTGTGTTCCAAAGATGCC	01T176A	GCCATCTTGGAAACCAACCCGCCCA		
01T178L	CTGTGAATAGCCACTACTCTT	01T178R	CATAAGAAAGTTACCAGTACATC	01T178E	GCTGTGTAACATCTCTCAGTTTCTATTAGG	01T178A	GCATTAATGAAACTACTAGGATTTAAACATC		
01T180L	TACCAGATTAGGCTCAATATCTA	01T180R	ACATAAGATTTGGGTGTGTTGT	01T180E	CTTCTGAAGCTGGGAGTGTGCAATCC	01T180A	GGATTTCTCAGCTCTCTCTGAGG		

Page 2

Table II

SNP	Left Primer			Right Primer			Labeled Probe			Probe on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')
01T182L	01T182L	CATGCTTTGTCAKAGKACATTC	01T182R	AGGTGCTCAAGTGAAGACAA	01T182E	CGCTCTCCAAAAGAGCTATCACTCTCT	01T182E	CGCTCTCCAAAAGAGCTATCACTCTCT	01T182A	AGGAAGTGAATAGCTCTTTTGGGAAGAC	01T182A	AGGAAGTGAATAGCTCTTTTGGGAAGAC
01T184L	01T184L	ACCAAGCTAGGGCATGGAC	01T184R	TCCATTCCACTGAAATTCATTC	01T184E	CTGCACCTGGCGAAGCTCCCACTATG	01T184E	CTGCACCTGGCGAAGCTCCCACTATG	01T184A	CATAGTGGGAGCTCTGCCAGTGCAG	01T184A	CATAGTGGGAGCTCTGCCAGTGCAG
01T185L	01T185L	TTCAAAATGTAGATCTCTCCGCTC	01T185R	CTAATTGGGAGTGCATCTCTCT	01T185E	TCTATTGGGACCTGGGTTCGATGGC	01T185E	TCTATTGGGACCTGGGTTCGATGGC	01T185A	GGCAATGCAACCCAGTGGCAATAA	01T185A	GGCAATGCAACCCAGTGGCAATAA
01T187L	01T187L	GGTCAATGGGCTGTGTGCTCT	01T187R	CTCCACAAAAGAACTCACT	01T187E	CTCAAAAGCTATCGATCCACCTGG	01T187E	CTCAAAAGCTATCGATCCACCTGG	01T187A	CCAGTGGGTGGATTCGATAGCTTTAGG	01T187A	CCAGTGGGTGGATTCGATAGCTTTAGG
01T188L	01T188L	TAAGAGTGAAGTCACTCTCTC	01T188R	TGTAAATGTGGGCTTGACAA	01T188E	GCCCTGGGTCTATGATCTTGGCAGT	01T188E	GCCCTGGGTCTATGATCTTGGCAGT	01T188A	TADTGGCAAACTCTATGACCAGGCC	01T188A	TADTGGCAAACTCTATGACCAGGCC
01T189L	01T189L	CCAAGATGGTGCATATGCAC	01T189R	CAGATGCTCACTCTCTATCC	01T189E	GGCACAAGGTTTCGTCTAAGAAATCTTTT	01T189E	GGCACAAGGTTTCGTCTAAGAAATCTTTT	01T189A	AAAAAGATTTTATGACAAAACCTGTGGC	01T189A	AAAAAGATTTTATGACAAAACCTGTGGC
01T192L	01T192L	AAACATTTTATGAGGCGAAGT	01T192R	TAATTTATGAGCTATCAACCGC	01T192E	CCGCGAGATCTATCTATAGCAATTTAGC	01T192E	CCGCGAGATCTATCTATAGCAATTTAGC	01T192A	GCTAAATGCTTATGAGATAGATCTCGG	01T192A	GCTAAATGCTTATGAGATAGATCTCGG
01T194L	01T194L	AGAGCTCTGAAGGACAGATC	01T194R	TCTTGAATTTGTGCAATTCAGT	01T194E	AGCAATGGCAACTGAGAGAGATA	01T194E	AGCAATGGCAACTGAGAGAGATA	01T194A	TATCTTCTCAAGTGTCCATCTCT	01T194A	TATCTTCTCAAGTGTCCATCTCT
01T196L	01T196L	TGCAAAATCTGTATATGCTT	01T196R	CTTACATGAAATATTCCTCTCAT	01T196E	CACACTTCCCAAGATACATCTATTAAGA	01T196E	CACACTTCCCAAGATACATCTATTAAGA	01T196A	TCTATAAATTTATGTATCTTGGAAAGTGT	01T196A	TCTATAAATTTATGTATCTTGGAAAGTGT
01T198L	01T198L	TGCATATGTGCTCTGTATG	01T198R	ATCTCTGTGCTATGGAGTGTAG	01T198E	GTAGGAATATTTGCTGTTAATAACTCTGTT	01T198E	GTAGGAATATTTGCTGTTAATAACTCTGTT	01T198A	AAACAGATTTTAAACAGAAATATCTCTAC	01T198A	AAACAGATTTTAAACAGAAATATCTCTAC
01T200L	01T200L	TTTACATGATGACACAAACA	01T200R	ATTTCTAGGTTGGGATATATAG	01T200E	CATCATAGAGTATAGGCCAATATGCA	01T200E	CATCATAGAGTATAGGCCAATATGCA	01T200A	TAATTTATGGCTTAATCTATCTATGATG	01T200A	TAATTTATGGCTTAATCTATCTATGATG
01T202L	01T202L	CTTCTTCAATTTGCTATGCTATC	01T202R	CTGCTTTATCCACCTTTGTATC	01T202E	TGTTCTCTCTTATTAAGAAATATTTGAGATA	01T202E	TGTTCTCTCTTATTAAGAAATATTTGAGATA	01T202A	TATCTCACATATATTTAATGATGAGAG	01T202A	TATCTCACATATATTTAATGATGAGAG
01T205L	01T205L	ATGCGCTCTCAAGATCTCT	01T205R	GCCAGATAGACTGCATATAGTAATA	01T205E	TTGCTCTTGATTTCAACAGTATTAAT	01T205E	TTGCTCTTGATTTCAACAGTATTAAT	01T205A	TAATAAACTGTGAATTCGAAGCAAA	01T205A	TAATAAACTGTGAATTCGAAGCAAA
01T206L	01T206L	AGATGCTGACCAAGCCTAAACT	01T206R	TGAGCTCTGTTGGGCCATCT	01T206E	TTAATCAAACTATGAGAGGGGCCA	01T206E	TTAATCAAACTATGAGAGGGGCCA	01T206A	TGGCGCTCTCTGAATCTTGATTA	01T206A	TGGCGCTCTCTGAATCTTGATTA
01T207L	01T207L	TGGCTATTTTGTGATCAACAAAT	01T207R	ACTGCTGACCAATGACATCTCT	01T207E	TCTCTGATCACAGCATATTAATCT	01T207E	TCTCTGATCACAGCATATTAATCT	01T207A	AGATTAATATAGTCTGTGATCAAGGA	01T207A	AGATTAATATAGTCTGTGATCAAGGA
01T208L	01T208L	AATCGAAGAGCATATCTAGAT	01T208R	TGGCAACAGCAAGCATCTAT	01T208E	AATAAGACGTAAATATTAATTAAGACTGC	01T208E	AATAAGACGTAAATATTAATTAAGACTGC	01T208A	CGAGTATAGTATAGTATTAATTAAGCTATT	01T208A	CGAGTATAGTATAGTATTAATTAAGCTATT
01T209L	01T209L	AGATTAATAGCATATCTGCTA	01T209R	ATGTTCAACAGCGTGTACTCT	01T209E	TCACAGAAATCTAGAGATCTGTTCTCT	01T209E	TCACAGAAATCTAGAGATCTGTTCTCT	01T209A	AGGAAACAGATCTATAGTCTTGTGTA	01T209A	AGGAAACAGATCTATAGTCTTGTGTA
01T211L	01T211L	GTAAATAGTACCTAAGATGTGTAG	01T211R	TGAAAAGCGCTGTACTATCT	01T211E	GATGTGTAGCATATATGTTTCTTAGGCTA	01T211E	GATGTGTAGCATATATGTTTCTTAGGCTA	01T211A	TAGCTTAAGAAACATTAATAGCTGTACATC	01T211A	TAGCTTAAGAAACATTAATAGCTGTACATC
01T213L	01T213L	ACCCAGAGGCAATGACAT	01T213R	GCCACAGACTGACGGCTA	01T213E	GACACATCTCTGACATCACTCAGC	01T213E	GACACATCTCTGACATCACTCAGC	01T213A	GCTGATGTCTGAGATTTGACGTGTC	01T213A	GCTGATGTCTGAGATTTGACGTGTC
01T217L	01T217L	TTAATGAGAAATGACCAATG	01T217R	ATTTCAATCTGAGATCTCTAT	01T217E	GCCCATAGAGTATATTAATTAAGCTCA						

Table II

SNP	Left Primer			Right Primer			Probe on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name
01T268I.	01T268I.	TTGTGTGATGGATATCTT	01T268R	TGATCAGAGACATCTTTTA	01T268E	CATGCACATCTTATGATATACAAA	01T268A	TTGTTACATCATAGATGTGCAGTG	
01T270I.	01T270I.	GGGGACTGTGCTCTGCTAC	01T270R	CAATACAGTCCCAATCCCTAGT	01T270E	CCACTGATCTCTTATGATTCGGTGAA	01T270A	TTCCAGGGCATTAATGGAATGATGATGG	
01T271I.	01T271I.	ATTGAGAGAGAAAAGAACAAAGT	01T271R	GTAAAGTCCCAAGTGGGTGAC	01T271E	TAAAGGTGCCAAGAGCTGCAATC	01T271A	GATTGCAGCTCTTGGCACCTGTTA	
01T272I.	01T272I.	CTGAGCTCTTCCCTCAACAT	01T272R	TCAATTAATTTTCCATAGATGGTA	01T272E	GATCAAGCTCTTCCCATTTTAAAGTAAT	01T272A	ATTACTTTTAAATGGGAAAGCTTGTATC	
01T273I.	01T273I.	CCGAGCACTTAATATATAGACAG	01T273R	TTAAATAGTCTGCTGCTGACT	01T273E	GGAAGCAAAAATATGAAATAAAAGATC	01T273A	GATCTTTTATCTCTATTTTGTGCTTCC	
01T274I.	01T274I.	CAAACCTGAGGACTCAATCT	01T274R	TTCTCCCTATCTCCCTCA	01T274E	GCTGCTGATCTGATGCTTCCAAAGGTAA	01T274A	TTACCTTTGTGAGCATCAGATACGACGC	
01T275I.	01T275I.	CGCAAGCTGAGAGACGGCTGG	01T275R	GGCAGCTGTTTCTTGCAAT	01T275E	GCTGCTGACTGTTTCAATGAGGCCATAA	01T275A	TATGGCTCTTAATTAACAGATGCGACG	
01T276I.	01T276I.	GGTGAATCAGGAAGATCTTAAGT	01T276R	CTCTCTCGAAGTCTGTAGGAG	01T276E	CTTCTTAATCTGCTATGCTTTAGTTGAG	01T276A	CTAACATAGCATATGACGATTAAGGAAG	
01T277I.	01T277I.	GCTTGCTGCTGCTCTCTCTGCTG	01T277R	GGTTTTCGCACTGGGGTCTGGA	01T277E	CCTCAGGCTGAGGCTCAGAGGGGA	01T277A	TCCCTCTTAGGCTCTGACGCTGAGG	
01T278I.	01T278I.	ACCATCAGATCTCATAGAGACT	01T278R	CTGTGCTCTCAAAAATCTATCT	01T278E	CCTCTATGATCTCAATCTCTCCACTGGTCC	01T278A	CGACCAAGTGGAGTAAATTAATCATAGAGG	
01T279I.	01T279I.	AGGACTGCCATTTCTTAATTC	01T279R	TCCACCTGGGGTGGCTTGC	01T279E	CGCGCGGAGAGCTGGGATCGTG	01T279A	CAGATCTAGGCTCTCTCTATCTTCT	
01T280I.	01T280I.	GTAAGAACATGAACTAAATAAAGT	01T280R	CTCTCTTAGAGAGCTATATGTA	01T280E	GAACAGACTACTAATACACTAGAGACCA	01T280A	CGACCAAGTGGAGTAAATTAATCATAGAGG	
01T281I.	01T281I.	AGCCGTGGTCTGGGACGGAACGA	01T281R	CTGCTTCTAGAGAGCTATATGTA	01T281E	GAACAGACTACTAATACACTAGAGACCA	01T281A	CGACCAAGTGGAGTAAATTAATCATAGAGG	
01T282I.	01T282I.	GTAGAACATGAACTAAATAAAGT	01T282R	TCCACCTGGGGTGGCTTGC	01T282E	CGCGCGGAGAGCTGGGATCGTG	01T282A	CAGATCTAGGCTCTCTCTATCTTCT	
01T283I.	01T283I.	GGTTTACGATTTCTCTCAA	01T283R	CTGCTTCTAGAGAGCTATATGTA	01T283E	GAACAGACTACTAATACACTAGAGACCA	01T283A	CGACCAAGTGGAGTAAATTAATCATAGAGG	
01T284I.	01T284I.	GGTTTACGATTTCTCTCAA	01T284R	CTGCTTCTAGAGAGCTATATGTA	01T284E	GAACAGACTACTAATACACTAGAGACCA	01T284A	CGACCAAGTGGAGTAAATTAATCATAGAGG	
01T285I.	01T285I.	GGTTTACGATTTCTCTCAA	01T285R	CTGCTTCTAGAGAGCTATATGTA	01T285E	GAACAGACTACTAATACACTAGAGACCA	01T285A	CGACCAAGTGGAGTAAATTAATCATAGAGG	
01T286I.	01T286I.	GGTTTACGATTTCTCTCAA	01T286R	CTGCTTCTAGAGAGCTATATGTA	01T286E	GAACAGACTACTAATACACTAGAGACCA	01T286A	CGACCAAGTGGAGTAAATTAATCATAGAGG	
01T287I.	01T287I.	GGTTTACGATTTCTCTCAA	01T287R	TATACCTTCTCTCCCACTCTC	01T287E	CAAGAAGAAAATAAACCCTTCTAAGAG	01T287A	CTTCTGAAAAGGTTATTTCTTCTCTTG	
01T288I.	01T288I.	GTGAGCATTTCAAGATCTTCTCA	01T288R	TTCTCCGTTTAATAGACATCTCT	01T288E	ATAAATAAGTAAGTATTTTAAATAAGAGTT	01T288A	AACCTCTATTTTAAATCTTATCTTCTTAT	
01T289I.	01T289I.	GTATGCTATTAACACATTAATCG	01T289R	GAAATGCACATTTTAAGCTGATTC	01T289E	GTATATTCCTATCGATAAATAATCTCTTAA	01T289A	TTAAGAGATATTTTATTCGAAATGGAATATG	
01T290I.	01T290I.	CCCAATCTAAATGTACATCAACT	01T290R	GAATGCACATTTTAAGCTGATTC	01T290E	GTATATTCCTATCGATAAATAATCTCTTAA	01T290A	TTAAGAGATATTTTATTCGAAATGGAATATG	
01T291I.	01T291I.	ACTATCTGTTCTAAGGTGTGAC	01T291R	GAATGCACATTTTAAGCTGATTC	01T291E	GTATATTCCTATCGATAAATAATCTCTTAA	01T291A	TTAAGAGATATTTTATTCGAAATGGAATATG	
01T292I.	01T292I.	ACTATCTGTTCTAAGGTGTGAC	01T292R	GAATGCACATTTTAAGCTGATTC	01T292E	GTATATTCCTATCGATAAATAATCTCTTAA	01T292A	TTAAGAGATATTTTATTCGAAATGGAATATG	
01T293I.	01T293I.	ACTATCTGTTCTAAGGTGTGAC	01T293R	GAATGCACATTTTAAGCTGATTC	01T293E	GTATATTCCTATCGATAAATAATCTCTTAA	01T293A	TTAAGAGATATTTTATTCGAAATGGAATATG	
01T294I.	01T294I.	ACTATCTGTTCTAAGGTGTGAC	01T294R	GAATGCACATTTTAAGCTGATTC	01T294E	GTATATTCCTATCGATAAATAATCTCTTAA	01T294A	TTAAGAGATATTTTATTCGAAATGGAATATG	
01T295I.	01T295I.	ACTATCTGTTCTAAGGTGTGAC	01T295R	GAATGCACATTTTAAGCTGATTC	01T295E	GTATATTCCTATCGATAAATAATCTCTTAA	01T295A	TTAAGAGATATTTTATTCGAAATGGAATATG	
01T296I.	01T296I.	ACTATCTGTTCTAAGGTGTGAC	01T296R	GAATGCACATTTTAAGCTGATTC	01T296E	GT			

Table 11



SNP	Left Primer			Right Primer			Name	Sequence (from 5' to 3')			Labeled Probe			Probe on Slide				
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')		Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
01T4251	01T4251	GCCTTGTAAGAAAGGGATG	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4252	GGTAAACAGGGTTACAGATACAGCTAC	01T4252A	GGTAAACAGGGTTACAGATACAGCTAC	01T4253	GTAGCTGTAGTGTGTAACCCCTGTTTACC	01T4253A	GTAGCTGTAGTGTGTAACCCCTGTTTACC
01T4256L	01T4256L	ATGTGCTCTCCCAAGGATACAGAT	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4256	AGTAAAGCCGGGTGTGGTGAAGTAC	01T4256A	AGTAAAGCCGGGTGTGGTGAAGTAC	01T4257	GTACCTTACAGATCTAGCAATGAGGG	01T4257A	GTACCTTACAGATCTAGCAATGAGGG
01T4271L	01T4271L	ACTCTGCTGTATGATCAAGACAGC	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4271	CCCTTAGTACATCTTCCCTCT	01T4271A	CCCTTAGTACATCTTCCCTCT	01T4272	GTCTCTAGTGTGGAAGTAACTTACCC	01T4272A	GTCTCTAGTGTGGAAGTAACTTACCC
01T4281L	01T4281L	CGGTATATCCAGATGATCAATGATGA	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4281	AAACAGATCTTCCCTCT	01T4281A	AAACAGATCTTCCCTCT	01T4282	GTCTCTAGTGTGGAAGTAACTTACCC	01T4282A	GTCTCTAGTGTGGAAGTAACTTACCC
01T4291L	01T4291L	ACCCATCTTCAATACCAACT	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4291	TGCCATGCAATCCCAAAAGACT	01T4291A	TGCCATGCAATCCCAAAAGACT	01T4292	TCATCTGAAACCTGTGGTGTAGACA	01T4292A	TCATCTGAAACCTGTGGTGTAGACA
01T4251	01T4251	GCCTTGTAAGAAAGGGATG	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4252	GGTAAACAGGGTTACAGATACAGCTAC	01T4252A	GGTAAACAGGGTTACAGATACAGCTAC	01T4253	GTAGCTGTAGTGTGTAACCCCTGTTTACC	01T4253A	GTAGCTGTAGTGTGTAACCCCTGTTTACC
01T4256L	01T4256L	ATGTGCTCTCCCAAGGATACAGAT	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4256	AGTAAAGCCGGGTGTGGTGAAGTAC	01T4256A	AGTAAAGCCGGGTGTGGTGAAGTAC	01T4257	GTACCTTACAGATCTAGCAATGAGGG	01T4257A	GTACCTTACAGATCTAGCAATGAGGG
01T4271L	01T4271L	ACTCTGCTGTATGATCAAGACAGC	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4271	CCCTTAGTACATCTTCCCTCT	01T4271A	CCCTTAGTACATCTTCCCTCT	01T4272	GTCTCTAGTGTGGAAGTAACTTACCC	01T4272A	GTCTCTAGTGTGGAAGTAACTTACCC
01T4281L	01T4281L	CGGTATATCCAGATGATCAATGATGA	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4281	AAACAGATCTTCCCTCT	01T4281A	AAACAGATCTTCCCTCT	01T4282	GTCTCTAGTGTGGAAGTAACTTACCC	01T4282A	GTCTCTAGTGTGGAAGTAACTTACCC
01T4291L	01T4291L	ACCCATCTTCAATACCAACT	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4291	TGCCATGCAATCCCAAAAGACT	01T4291A	TGCCATGCAATCCCAAAAGACT	01T4292	TCATCTGAAACCTGTGGTGTAGACA	01T4292A	TCATCTGAAACCTGTGGTGTAGACA
01T4251	01T4251	GCCTTGTAAGAAAGGGATG	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4252	GGTAAACAGGGTTACAGATACAGCTAC	01T4252A	GGTAAACAGGGTTACAGATACAGCTAC	01T4253	GTAGCTGTAGTGTGTAACCCCTGTTTACC	01T4253A	GTAGCTGTAGTGTGTAACCCCTGTTTACC
01T4256L	01T4256L	ATGTGCTCTCCCAAGGATACAGAT	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01T4300A	CTCTAAAGCTTGGTGTAGTATATACAGACC	01T4256	AGTAAAGCCGGGTGTGGTGAAGTAC	01T4256A	AGTAAAGCCGGGTGTGGTGAAGTAC	01T4257	GTACCTTACAGATCTAGCAATGAGGG	01T4257A	GTACCTTACAGATCTAGCAATGAGGG
01T4271L	01T4271L	ACTCTGCTGTATGATCAAGACAGC	01T4230L	TCAATGACAAATGAAGCTGTGA	01T4230R	CGGCTCAAAAGATGTAAAGGTGGCAC	01T4300E	GGTCTGATATCTAGTACCAAGCTTAAAG	01									

Table II



SNP	Left Primer			Left Primer			Right Primer			Right Primer		
	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')
16-0121	16-0121R	GTCTGAGTCTCGAGTATGTGAT	16-0121R	TGCTCATCATCTCTGTCTGGTA	16-0121E	ACCTGCTCTTTTGTGGACATCTGCTCTCT	16-0121A	AGGAGAGCAGAGATGTCACAAAGACAGGT	16-0121A	AGGAGAGCAGAGATGTCACAAAGACAGGT	16-0121A	AGGAGAGCAGAGATGTCACAAAGACAGGT
16-0131	16-0131R	CCCTTCTCTCCCAKCTGGGA	16-0131R	CATCCCAAACTACACAGAGTCG	16-0131E	ADACTCTGCGACCCAGGTGTGGGCT	16-0131A	AGGCTCAGCTGGGTGCGGACAGTCT	16-0131A	AGGCTCAGCTGGGTGCGGACAGTCT	16-0131A	AGGCTCAGCTGGGTGCGGACAGTCT
16-0141	16-0141R	ACATCTGTGGACATTTGAGACAA	16-0141R	GTGAGTGGCCAGGGTCTTGG	16-0141E	AGGCGAGTGAATAACTCTGCTGACACACTA	16-0141A	TGACTCAGTGAAGTATTTTCACTGCCCT	16-0141A	TGACTCAGTGAAGTATTTTCACTGCCCT	16-0141A	TGACTCAGTGAAGTATTTTCACTGCCCT
16-0161	16-0161R	CATCTGTGGACATTTGAGACAA	16-0161R	ATGAGTGGTGGTCTGTGGGA	16-0161E	TGACACTTAAATCAGAGACTAACCATGTG	16-0161A	CACATGTTAGCTCTCGATTTAGGTGTCA	16-0161A	CACATGTTAGCTCTCGATTTAGGTGTCA	16-0161A	CACATGTTAGCTCTCGATTTAGGTGTCA
16-0171	16-0171R	AAACCAAGACAGCTGAAGCGGGC	16-0171R	AGGCTGGTGGCCCATATATGGGTAAAT	16-0171E	GGTGTGGGAGAGACAGAGATCTCGGT	16-0171A	ACGCGAGGATCTCTGTCTCTCCCGACACC	16-0171A	ACGCGAGGATCTCTGTCTCTCCCGACACC	16-0171A	ACGCGAGGATCTCTGTCTCTCCCGACACC
16-0181	16-0181R	TAATCCAAACAACCTAGAGGCTTAAT	16-0181R	TTAGTAGCAGCAGTAGAGGCG	16-0181E	AAAGCTGCAGTAGCAGATGATCTTTAATTC	16-0181A	GAATTAAGAAATCATCTGCTACTGACGCTT	16-0181A	GAATTAAGAAATCATCTGCTACTGACGCTT	16-0181A	GAATTAAGAAATCATCTGCTACTGACGCTT
Probe on Slide												
SNP	Left Primer			Left Primer			Right Primer			Right Primer		
	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')	Name	Sequence (5' to 3')
16-0201	16-0201R	TACTGCGACGACGCCATTCTA	16-0201R	AACCGAGATGAGCTGCTTAATAGTA	16-0201E	TCTGAGCTTGCTGCTCTTTCCAGGCCAGG	16-0201A	CTTGCTCTGGAAGAGAGAGGCGAGCTGTAGAA	16-0201A	CTTGCTCTGGAAGAGAGAGGCGAGCTGTAGAA	16-0201A	CTTGCTCTGGAAGAGAGAGGCGAGCTGTAGAA
16-0211	16-0211R	TACATGAGGCGCTTATCCCGGC	16-0211R	TGTGCTTGATCTGCTGTGTAGAGAC	16-0211E	TCTGTGGAAGAGGTGATGCTGTCTGGGAAA	16-0211A	TTTCCATAGACAGAGTCCATTTCCACCAAG	16-0211A	TTTCCATAGACAGAGTCCATTTCCACCAAG	16-0211A	TTTCCATAGACAGAGTCCATTTCCACCAAG
16-0221	16-0221R	GGAATGCACTGTATCCCAAC	16-0221R	CATCTCACTTACTTACTAATTTGCT	16-0221E	AACATGTACTCTCGAGGTGATATAGTCT	16-0221A	AGACTAATAAGACTCCGAGATACATGTT	16-0221A	AGACTAATAAGACTCCGAGATACATGTT	16-0221A	AGACTAATAAGACTCCGAGATACATGTT
16-0231	16-0231R	TCTCTCTCTGACTTCTGGAT	16-0231R	TGTGTGCAAAATTGGCTGGTA	16-0231E	TTACATAGAAGCCCGGTTCTCAGACCTT	16-0231A	AGGGTCTGAGAAACGGGGTGTCTTATGTAA	16-0231A	AGGGTCTGAGAAACGGGGTGTCTTATGTAA	16-0231A	AGGGTCTGAGAAACGGGGTGTCTTATGTAA
16-0241	16-0241R	AGCGCGGCTCTCTCTCATAGT	16-0241R	GGAGACAGCACTCTCTCTTAC	16-0241E	TAATTTAGGAGAGTGAATTTGGTGTGATAC	16-0241A	GTATCTCCACAGCAATCATGCTCTATAAAT	16-0241A	GTATCTCCACAGCAATCATGCTCTATAAAT	16-0241A	GTATCTCCACAGCAATCATGCTCTATAAAT
16-0251	16-0251R	ATCTGTGGTCTCTCTCTACAC	16-0251R	GGAATTAAGGCTTGTGTGTGACA	16-0251E	CATCTGCCACCACTCTCCACCAAGT	16-0251A	AGCTGTGGTAAGAGTGTGTGCCAGGTG	16-0251A	AGCTGTGGTAAGAGTGTGTGCCAGGTG	16-0251A	AGCTGTGGTAAGAGTGTGTGCCAGGTG
16-0261	16-0261R	TTCCACATATTAGGCGAAGTG	16-0261R	TGGAATGATAGGGGTAGTG	16-0261E	GATGTTGCCCTTGTGCGAATCCAGGC	16-0261A	GCTTGGACTCCGACAAAGGCGACATC	16-0261A	GCTTGGACTCCGACAAAGGCGACATC	16-0261A	GCTTGGACTCCGACAAAGGCGACATC
16-0281	16-0281R	TGCCCCAGGGCTTATACATAGT	16-0281R	CTGTGCGCTCTGCAAGAAAGTCC	16-0281E	GTCCCTGATGGACTGGATGATGCTGAAGT	16-0281A	AGCTTTCAGCTTCCAGTATCTCATAGGAC	16-0281A	AGCTTTCAGCTTCCAGTATCTCATAGGAC	16-0281A	AGCTTTCAGCTTCCAGTATCTCATAGGAC
16-0311	16-0311R	TCCCTCTCTAATGTGTCAATG	16-0311R	CAAGTGGATCCGCAAGAAATTTCT	16-0311E	CCAGGAATGTGCATGCTGTGTGTACAGG	16-0311A	CCTGACACACCCAGTATGCAATCTCTGG	16-0311A	CCTGACACACCCAGTATGCAATCTCTGG	16-0311A	CCTGACACACCCAGTATGCAATCTCTGG
16-0321	16-0321R	TGAGCGAGTCTGTGAAATCTT	16-0321R	TTATACATATCAGAGCGGAAA	16-0321E	AAATTCGAAGTCTCTCTCTTAAGGGCAGG	16-0321A	CTGCGCTTAAGAGAGAACTTGGAAATTT	16-0321A	CTGCGCTTAAGAGAGAACTTGGAAATTT	16-0321A	CTGCGCTTAAGAGAGAACTTGGAAATTT
16-0331	16-0331R	GCAATCTACTAGAAATGGCAT	16-0331R	TGGAAGAAATTTTCTCTCAATC	16-0331E	GGGAGCAGGGCTTAATCTTATGTGCTTA	16-0331A</					

Table II



SNP	Left Primer			Right Primer			Probe on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
16-0751	16-0751L	TTTAACTCAGTCTGAGTTTGTGTTA	16-0751R	GTGTTCTGCCATACAGUQTAT	16-0751E	TTAAGTTGTATTGCTGTCAATTGCATCTG	16-0751A	CAQATGCAATTCAGCAGCAATAAACAATTAA	
16-0761	16-0761L	TGACTCTGCTGCTGGTGGTGGATTTCT	16-0761R	TTTCTCAGAAATTCACATCCCTG	16-0761E	CCCTGCTCTCAGACCTCATCTGTCAACC	16-0761A	CGGTGCAAGATAGGGGCTGTGAGAAAGCAGG	
16-0771	16-0771L	CTTGCGGAGAGGTTGTCATGAT	16-0771R	TCCAGAGCAATTTGCTCTTACCA	16-0771E	ACAGAACTTAGATCTAGCTCTGCTGCAACC	16-0771A	CGTGTCCAGGAAGCTCAGATCTAAGTCTGT	
16-0791	16-0791L	TATGAAATGAAATACAGCAT	16-0791R	TTAGAAGTTTGGATGACAGCAGGGCT	16-0791E	AGGATGAAAGTCTTCAAGTGAAGATCA	16-0791A	TGATTTCTTCACTGAAGACATCTCATCTCT	
16-0801	16-0801L	ATCAAAAGCCCTCAGCAATCT	16-0801R	CTCCGCGCAGCAACCAAGATTC	16-0801E	CATCAGCAGTATAGCTGCTGATGACGGGT	16-0801A	ACCCTGACTCAGGCAATGATACTGCTGATG	
16-0811	16-0811L	ACGCTTACAGCTGCTGCTGCTGCTG	16-0811R	CATTTAGCTCTCTTGGCAGAAC	16-0811E	TGTGGAAGCCGCGAGAGTAGAGGCA	16-0811A	TGCTCTACTCTCGGCGCTCTCTCCACA	
16-0821	16-0821L	AAATTCAGGCTTTCACAAAG	16-0821R	CTGTTGCTTAATGAGGCTCC	16-0821E	CAGCTTGAATTTGCTGCTGCTGCTGAGCG	16-0821A	CGCTACCGGAGCAGCAATATACAGCTG	
16-0831	16-0831L	AGGAAATCAGAGCTGAAAT	16-0831R	GCCTAGCTCAGACCTGAGATTC	16-0831E	TAAATTTGGCAATATCTGCTCTTTCTAG	16-0831A	CTAGAAAGAGCAAGATATTTGCTCAATCTTA	
16-0861	16-0861L	TTGAGCTGGGGGCTCCCTCCG	16-0861R	ACCTCAGACAGCACTCTTGG	16-0861E	GAGGTGCGAGCTGCTGCTGCTGCTGCTG	16-0861A	GGGTGGGCACTCAGGCTGCACCTTC	
16-0871	16-0871L	GCAGGGAAGAGATGATCAAT	16-0871R	CAGGTGCTTGGTTAAGCAT	16-0871E	CATGGGTGGAAGGGGACAGGCTCC	16-0871A	GGAGGCTGCTCCCTTTTCAACCCCATG	
16-0881	16-0881L	AGTCCGAGGATGATAGGTAC	16-0881R	GGAAATGCTGCTCTCTGCTG	16-0881E	GAACCTCTGGGAGGCTCTGGGCTG	16-0881A	CCACCCAGGCTCTCCCGCAGGAGGCT	
16-0891	16-0891L	CATGACACTGATGAGGGCT	16-0891R	TTTGCAGGCTGACTCTCCAGATG	16-0891E	AGCTCTAGCTCTTCTCCCACTAGCAT	16-0891A	ATCTAGTTGTTGGGCAAGAACTAGACT	
16-0901	16-0901L	GGAATGGGAGGCTGGCCCTTA	16-0901R	TGAGGTGAGAGAGGAGCATC	16-0901E	GGACCTCAGGCACTTGAAGTGAACCTCAG	16-0901A	GTGAGGCTCACTCAAGTCTGCTGATGCTC	
16-0911	16-0911L	TTTGGGAGCAGCAACCTGGC	16-0911R	GATTAAGCACTGACAAACAACATGTA	16-0911E	ACAACCTTAAGTCTGGCATCAAGAAGACA	16-0911A	TCCTCTCTGCTCCAGACTTTACAGTTCT	
16-0921	16-0921L	GTTCATGTGCTCAATTAATCTGTTTAC	16-0921R	CCCTTTCAGAGCAGCACTTA	16-0921E	CAGCTTATTAATTAATCTGATGATGCTCA	16-0921A	TGCACTAATTAATGCTCCCAAGGCAATTA	
16-0931	16-0931L	CTCAACCTCCTCAATTAAGT	16-0931R	AGTTATTTTCCAGCAGCAACT	16-0931E	TTTGTGTGACTTCTCACTCTGAGAGGCT	16-0931A	TGCACTAATTAATGCTCCCAAGGCAATTA	
16-0941	16-0941L	ATCCAGAAATTAAGACAGGCTTA	16-0941R	GTTCCTTGGCTCTGATTAAGT	16-0941E	AGTTTACACTCTCAACTTAACCTAAGAGA	16-0941A	TCCTCTCAGAAATGGAAGTCAACAGCAAA	
16-0951	16-0951L	AGGGGAAGGAGAGCAATATG	16-0951R	TTTCTGCTGCTGCTGCTGCTGCTG	16-0951E	GGCTCAGGTGACTCAAGGAGGAAAGCACT	16-0951A	AGGTGCTTCTCTGCTGCTGCTGCTGCTG	
16-0961	16-0961L	TGCTTCCAGCTGCTGGGCTCAG	16-0961R	TCAGCAGGCTCAGAGATGGGG	16-0961E	TCTTACAAATGGAATTTCCCACTCAGACA	16-0961A	TCTTGGGATGGGAAATCACTTTTGTAGAA	
16-0971	16-0971L	AAOTGTAGATGCTCAGCTGGTA	16-0971R	TGCCCTCTGCTCTCTTCTG	16-0971E	TTCTACAAATGGAATTTCCCACTCAGACA	16-0971A	TCTTGGGATGGGAAATCACTTTTGTAGAA	
16-0981	16-0981L	AGATGTGCTGCTATTAACACAGCT	16-0981R	CAGTGTGTTTGTGGAAGT	16-0981E	GGAAAGTTAGAAAGCATGCTCTAGTGTG	16-0981A	CACTACGATGATGCTCTTCTTCTTATGACC	
16-0991	16-0991L	GGAGAAAGAAAGAAAGAAAGCTAAT	16-0991R	GACCATGTGCTGGCAGAAAT	16-0991E	TTGCTCTCTTCTGGAAGTTCCCAAATGCTCT	16-0991A	AGGCAATTTGGAATCTTCDAAAGAGAGCAAA	
16-1001	16-1001L	ATTAGGATCTCTTGGTCTG	16-1001R	CATGGGCTCAGCTCTGTTCCAGAT	16-1001E	TGGCAGGCTGGGCAAGGAGAAATGC	16-1001A	CACTTCTCTGCTCCCAAGCTCTCCA	
16-1011	16-1011L	CACAGCTTGTGCTTGTGTTGCT	16-1011R	ATTAGTACAGATTTGTGTGATGTA	16-1011E	CTATTACTAGGCACTACTGATGCTGCTGA	16-1011A	TCAGGCTACAGTATGATGCTCAGTAATAAG	
16-1021	16-1021L	GCTGTGCTCGGAGCCAGCCAGCG	16-1021R	TGCAACCTGTGAGGBCACAAA	16-1021E	CACAGCCTCTGCTCCCAACCGCA	16-1021A	TGAGTGGGTGGCAGAGGCTGTG	
16-1031	16-1031L	CAGCTCTGGAATTAATGAG	16-1031R	TTTACACAGCAGGCAAGATAAT	16-1031E	CCCTGGATGTTTCCCACTCATCTCTATAC	16-1031A	TGTAATAGGATGATGGGCAAGACTCCAGCG	
16-1041	16-1041L	CAGCTGTCTCTATCTTTTAC	16-1041R	TAGCTTCCCAAAACATCTTTCTTA	16-1041E	GTCAAGTCTTTTGTACGATGTGAATAA	16-1041A	TAATTTCACTCTGACAAAGGAACACTGAC	
16-1051	16-1051L	ATGAAAGCTGGGTGGTCTTTGGGTA	16-1051R	ATCAAGGCTCTTCAAGAACT	16-1051E	GGTAGGGTGCAGGGTAATGATTTGCTACCC	16-1051A	GGGTAGCAATCTATTACCTGCAACCTTAC	
16-1061	16-1061L	TCTCTGGGAGAGAGAGAACTAA	16-1061R	CTCTTGGGAGATAGTTTCTCTGTA	16-1061E	CCCTGTACCAACAGAGCAAGACAGATGC	16-1061A	CGATGTGCTCTGCTGTGTGTGTAACAGG	
16-1071	16-1071L	TGCGGCAAGCTGGAATGCG	16-1071R	CCGCCAGCCCTCTCACTCAGTA	16-1071E	ACTGATGTTAACTCAAGTGGCCAGTGC	16-1071A	CCAGTGGCCACTTGAGTTTACACTCAGGT	
16-1081	16-1081L	GCCTCAATGAACACATCAGCG	16-1081R	GGCAGGTAGTGTGCTGCTGCTG	16-1081E	TGGTGAAGGCCCAAGAAAGCTTGCTG	16-1081A	CAGACCAAGCTTCTTGCGGCTCTTCAACA	
16-1091	16-1091L	ACTTGTGCTGCTGCTCAATGTTA	16-1091R	GCACCAAGCCAGGCTCTCTGCTA	16-1091E	TAAACAGCAAGCAGGAGGCTGACTCTTA	16-1091A	TAGGAGCACTCTCTGCGGCTCTCTGTTA	
16-1101	16-1101L	GAACCTATTTGAACTGCTGCTGCTG	16-1101R	CTCTCTGCTTAATGCTTCTGAT	16-1101E	CTATGAAAGCACTAGGCTGTGCTCTCTTA	16-1101A	TAAAGGCAAGCTAGTTCCTCTGCTGCTG	
16-1111	16-1111L	CTACTGGGTTACATTGGAAGCCG	16-1111R	GGGAGCAACATGTAAGTTTGTGA	16-1111E	CTATGAAAGCACTAGGCTCTTGTCCCA	16-1111A	TGGGCAAAATGGGCTCAGTTTCAATAG	
16-1121	16-1121L	TCATATGCTGATGGCAATGCAACCT	16-1121R	GAAGGCAAGGCAAGCAAGAA	16-1121E	GAAGAGGCAAGCAAGTGTGCAATGCCCTG	16-1121A	CAGGCACTGGAATCTGCTGCTGCTTTC	
16-1131	16-1131L	TTTACATCTCTACCTCTGTACAC	16-1131R	TGAAGTGAATGGGAGCTCAT	16-1131E	ATTTCAAGGGAAGGATGTCAGACCAAG	16-1131A	ATTCCTCTCTCAGGCTCTCTCTGTAAT	
16-1141	16-1141L	GTCTCTCAGTGAACCAATATG	16-1141R	TTCTCTGATCAGCTGCTGCTG	16-1141E	ACAGTTGAGTTTCTCATGTTCCCTCTATTA	16-1141A	TAAATAGGGAACAATGAAAGAACTCACTGT	
16-1151	16-1151L	TGAAAGTCTTCTCTGGGTGCTGCTA	16-1151R	AAAGTGAATGAGTGAATGCTGCTG	16-1151E	CAGATGCTATGGAATGAGGATGGAAGACA	16-1151A	TGCTGCTGCTCAGCTCTCATCAGTACCTG	
16-1161	16-1161L	ACCAGTGGTCTGTTTCTGAT	16-1161R	TTATCTGCTGCCAGATGGGAC	16-1161E	CAGTTTCACTTACTGTTTGTAGACTCC	16-1161A	GGATTTCTACAAAAGATTAATGTGAACCTG	
16-1171	16-1171L	CAGCTAGACCACTAATCCTGGCTCA	16-1171R	TGCTGCTGCCAGATATCATCT	16-1171E	CTGCTGCTCTCAAGTTTCACTCAGCAGA	16-1171A	TGCTGCTGCTGAAATCTGAAAGGCAACAG	
16-1181	16-1181L	ATCGGCTGCTGCTACCGCTGA	16-1181R	TCTATTTCTTCTTCAAAATGTGAC	16-1181E	TGACGGGATGAAAGAAATGCTGACACAA	16-1181A	CTTGTGTCAGCACTTCTTCTATCCTCCGCA	
16-1191	16-1191L	GAGATTTTCTTCTCTCTCCCTCT	16-1191R	TGTGAATCTGCTCTCTATAGACT	16-1191E	GATCAATAGCCCAAGACATATTTGGGATG	16-1191A	CATCCCAAAATATGCTTTTGGCTATGGTC	
16-1201	16-1201L	AAAGGAAATACCAAGATGCTGCTG	16-1201R	CATCAGATGCTCTACTGCTCTCCG	16-1201E	CTTCTGCTGAGGCTCTCCCAAGAAAGCC	16-1201A	GGCTTTTTTGGGAGGCTGCTGAGCAGG	
16-1211	16-1211L	CAGTAAATCCAGGGCAGATGATG	16-1211R	TGGAAATATGGGTAGCTTGA	16-1211E	TGAGAAGTATTAAGATGCTCTCTCTCT	16-1211A	AGAGAGAGAGGGGATCTTAATAGTCTCA	
16-1221	16-1221L	CGGGGCAAAATATTACCAATC	16-1221R	GCCTAAAGATGATGCTGATG	16-1221E	TCTTCACTCCAGGCTCAGAGAGACACAC	16-1221A	TATAACTCTCTTGAGGCTGCGGATGAAAG	
16-1231	16-1231L	TAGACAAAGGATGAGATCTTGTG	16-1231R	GGCTAAAGTCTGCTGCTGCTG	16-1231E	ATTCAGTTTATTAAGATTTGTGTAGCA	16-1231A	ATGCTGCTGCTGGGCTTGTATGACTTA	
16-1241	16-1241L	GCTGGAATTTACACTGATGATGACT	16-1241R	ACATTTATGAGCAGCTGCTGGAAC	16-1241E	GGAGCTCAGCAAGGTAATCTGCTG	16-1241A	TATAACTCTCTTGAGGCTGCGGATGAAAG	
16-1251	16-1251L	CTCAAGTGAACATGAAACCTTA	16-1251R	TCTAGCCAGGAGCAAAATCTGCT	16-1251E	TCTAGCCAGGAGCAAAATCTGCT	16-1251A	TATAACTCTCTTGAGGCTGCGGATGAAAG	
16-1261	16-1261L	ATACCATAGCAGTCCCAACAC	16-1261R	GGGCTGCTGGGAGAGAAAGAT	16-1261E	TTCGAGCAACCCCGAGCCACGACCT	16-1261A	ATGCTGCTGCTGGGCTTGTATGACTTA	
16-1271	16-1271L	CTACTGAATCAAGAACTCTGGC	16-1271R	GGACACATGAACTCTAGAT	16-1271E	TAGGCGGCAAGGATCTCTTCTCAAACTGAG	16-1271A	CTCAGTTTGAAGAGGATCCCTGTGCCCTTA	
16-1281	16-1281L	GTTCCTGTGCTGCTGCTGCTGCTG	16-1281R	TCTAAGTCTCTTCTGAAAGGCTTA	16-1281E	CACTCTGTGCTGCTGCTATCTCATCTCAT	16-1281A	ATGATTAAGATGAGATGCAACACAGATG	
16-1291	16-1291L	TTGCTATCATGTAGCTAGAGCTGAT	16-1291R	CATCATCAGGGCTTCAACCTCTGA	16-1291E	GAGACAGGCTGAGACCATGCAAGGCACTT	16-1291A	AATGTGCTCTCTCATGCTCTCATCTGCTTC	
16-1301	16-1301L	CGCGGCCATTTCTATTGGGCTA	16-1301R	TCCAGAGAGCTGGCTTTTAAACCT	16-1301E	GAAATATGCTGCTGCTGCTTCTTCAAGCT	16-1301A	AGTTGCTCTCTCTCATGCTCTCATCTGCTTC	

SNP	Left Primer			Right Primer			Probe on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')			
16-1311	16-1311	GCTTGGATTACTGTTGTTAT	16-1311	GGCTGCTCTCAACCTCCAAAC	16-1311E	TCTGAAGCTTTTGAATAACCTGAGGAG			
16-1321	16-1321	TTCCAGATTTTGTGATCT	16-1321	TCCTGGGAGGAGAAATGAC	16-1321E	GTGGCATTCATTTGAATGAAGGTTGACGC			
16-1331	16-1331	AGACCCAGGTGTTGATCATAGTAT	16-1331	ACTCATGTGTGTTTGAAT	16-1331E	TAGCTTAGAAGTGGGACAGGTTTAT			
16-1341	16-1341	TGGTGGCTGGAATATATCT	16-1341	TTGGCTCTACAGATCTGGGCG	16-1341E	AGCCAGCTCTG CAGCAGCTCTCTTGGAA			
16-1351	16-1351	ACTTTCCATGAGAGATAT	16-1351	CTTACACCAAGGGGTTGGGTGA	16-1351E	CAGCTGTTTGAATAGTGTCTATAGATGA			
16-1361	16-1361	GGATTCCTATGTTTCACTTCCG	16-1361	AGGAGGTGAGGAGCTACTTTC	16-1361E	CATTCTGCAAGAGCCCAAGCCTCC			
16-1371	16-1371	CAGCTGTTTAAAGAAATTCG	16-1371	ACCACAGCAGCTCTACGAT	16-1371E	TGGGATTTGGCCCTGTTAGCTGAGGAG			
16-1381	16-1381	GAGACCACTCTCTGTGACCTCA	16-1381	TTCTGGGCCACCAAGGGGAACC	16-1381E	CAGGTAGGATGTTTGTGATCAAGGATGTC			
16-1411	16-1411	GCTGACACTGCTCTTCCCGGCA	16-1411	TGCGGAAAGAGGGGCTGGGATAG	16-1411E	TGGCATAGCTCTGTTTGAAGCATGAGCTTG			
16-1421	16-1421	GGGTGGCAGAGGCTCTGGGTA	16-1421	GAGCCGCTGCTGCTCTGGTGC	16-1421E	GCCTAGGGGCTCTGACAGCAAGCA			
16-1431	16-1431	CATCAGCTAGGAGCAAGCTCTG	16-1431	CAGAGAGAGCCCTCTGCT	16-1431E	GGCAGCATCTCTCTAGAGAGCCAGGAA			
16-1441	16-1441	AGACCACTGCTGCTGACAGAGCTA	16-1441	GGGTGAGACGCTCTGGGTG	16-1441E	GGTGTGGGATTCAGTCTCCATTTCTTA			
16-1451	16-1451	GGTGGCCCAAGGTTTAGGAG	16-1451	AGAGGTTGGGAGAGGGGCTTA	16-1451E	CTGGCTGGTTTAGTACCGGGTAACTTTTC			
16-1461	16-1461	GAATTTGGTTGGATCTGGGTA	16-1461	CTCTGACCAATGGTGTGGTGA	16-1461E	TGAGGATCTCTAGCAAGTAAAGGATGGTG			
16-1471	16-1471	TCAGAGACAAAGCTGAGGATA	16-1471	CACCTATGATAGGATCTCATTA	16-1471E	GTATTCGATACCTCTGATATGCTCTGG			
16-1481	16-1481	AGCCAGACTGAACACCTGTA	16-1481	GACCTAGGAGATTAACCTGAT	16-1481E	TCAGTGTTCACCAATATGCTGAGAGGAG			
16-1491	16-1491	TTCCCGACTCTCTGTATC	16-1491	TGAACAGGGCAGCAAGCAACG	16-1491E	CTGTATCTCTCAACATATCAAGTGAAG			
16-1501	16-1501	TGGGTACCTCTGGGGAGAAATG	16-1501	CAGCCAGACTCGATCCCTCTATC	16-1501E	GAACTAACCTCAAGGCAAGGCTGATAT			
16-1511	16-1511	TCGCACTCTACCTCTTACCTG	16-1511	CAGGCTGGGAGATCTGGG	16-1511E	CAGACCCAGGGTGAAGCCAGGGGGA			
16-1521	16-1521	TCGCACTCTACCTCTTACCTG	16-1521	CAGGCTGGGAGATCTGGG	16-1521E	CGGCTATCTCTAGCAAGTATGGAAGGC			
16-1531	16-1531	TCGCACTCTACCTCTTACCTG	16-1531	CAGGCTGGGAGATCTGGG	16-1531E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1541	16-1541	TCGCACTCTACCTCTTACCTG	16-1541	CAGGCTGGGAGATCTGGG	16-1541E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1551	16-1551	TCGCACTCTACCTCTTACCTG	16-1551	CAGGCTGGGAGATCTGGG	16-1551E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1561	16-1561	TCGCACTCTACCTCTTACCTG	16-1561	CAGGCTGGGAGATCTGGG	16-1561E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1571	16-1571	TCGCACTCTACCTCTTACCTG	16-1571	CAGGCTGGGAGATCTGGG	16-1571E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1581	16-1581	TCGCACTCTACCTCTTACCTG	16-1581	CAGGCTGGGAGATCTGGG	16-1581E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1591	16-1591	TCGCACTCTACCTCTTACCTG	16-1591	CAGGCTGGGAGATCTGGG	16-1591E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1601	16-1601	TCGCACTCTACCTCTTACCTG	16-1601	CAGGCTGGGAGATCTGGG	16-1601E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1611	16-1611	TCGCACTCTACCTCTTACCTG	16-1611	CAGGCTGGGAGATCTGGG	16-1611E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1621	16-1621	TCGCACTCTACCTCTTACCTG	16-1621	CAGGCTGGGAGATCTGGG	16-1621E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1631	16-1631	TCGCACTCTACCTCTTACCTG	16-1631	CAGGCTGGGAGATCTGGG	16-1631E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1641	16-1641	TCGCACTCTACCTCTTACCTG	16-1641	CAGGCTGGGAGATCTGGG	16-1641E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1651	16-1651	TCGCACTCTACCTCTTACCTG	16-1651	CAGGCTGGGAGATCTGGG	16-1651E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1661	16-1661	TCGCACTCTACCTCTTACCTG	16-1661	CAGGCTGGGAGATCTGGG	16-1661E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1671	16-1671	TCGCACTCTACCTCTTACCTG	16-1671	CAGGCTGGGAGATCTGGG	16-1671E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1681	16-1681	TCGCACTCTACCTCTTACCTG	16-1681	CAGGCTGGGAGATCTGGG	16-1681E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1691	16-1691	TCGCACTCTACCTCTTACCTG	16-1691	CAGGCTGGGAGATCTGGG	16-1691E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1701	16-1701	TCGCACTCTACCTCTTACCTG	16-1701	CAGGCTGGGAGATCTGGG	16-1701E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1711	16-1711	TCGCACTCTACCTCTTACCTG	16-1711	CAGGCTGGGAGATCTGGG	16-1711E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1721	16-1721	TCGCACTCTACCTCTTACCTG	16-1721	CAGGCTGGGAGATCTGGG	16-1721E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1731	16-1731	TCGCACTCTACCTCTTACCTG	16-1731	CAGGCTGGGAGATCTGGG	16-1731E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1741	16-1741	TCGCACTCTACCTCTTACCTG	16-1741	CAGGCTGGGAGATCTGGG	16-1741E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1751	16-1751	TCGCACTCTACCTCTTACCTG	16-1751	CAGGCTGGGAGATCTGGG	16-1751E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1761	16-1761	TCGCACTCTACCTCTTACCTG	16-1761	CAGGCTGGGAGATCTGGG	16-1761E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1771	16-1771	TCGCACTCTACCTCTTACCTG	16-1771	CAGGCTGGGAGATCTGGG	16-1771E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1781	16-1781	TCGCACTCTACCTCTTACCTG	16-1781	CAGGCTGGGAGATCTGGG	16-1781E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1791	16-1791	TCGCACTCTACCTCTTACCTG	16-1791	CAGGCTGGGAGATCTGGG	16-1791E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1801	16-1801	TCGCACTCTACCTCTTACCTG	16-1801	CAGGCTGGGAGATCTGGG	16-1801E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1811	16-1811	TCGCACTCTACCTCTTACCTG	16-1811	CAGGCTGGGAGATCTGGG	16-1811E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1821	16-1821	TCGCACTCTACCTCTTACCTG	16-1821	CAGGCTGGGAGATCTGGG	16-1821E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1831	16-1831	TCGCACTCTACCTCTTACCTG	16-1831	CAGGCTGGGAGATCTGGG	16-1831E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1841	16-1841	TCGCACTCTACCTCTTACCTG	16-1841	CAGGCTGGGAGATCTGGG	16-1841E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1851	16-1851	TCGCACTCTACCTCTTACCTG	16-1851	CAGGCTGGGAGATCTGGG	16-1851E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1861	16-1861	TCGCACTCTACCTCTTACCTG	16-1861	CAGGCTGGGAGATCTGGG	16-1861E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1871	16-1871	TCGCACTCTACCTCTTACCTG	16-1871	CAGGCTGGGAGATCTGGG	16-1871E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1881	16-1881	TCGCACTCTACCTCTTACCTG	16-1881	CAGGCTGGGAGATCTGGG	16-1881E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1891	16-1891	TCGCACTCTACCTCTTACCTG	16-1891	CAGGCTGGGAGATCTGGG	16-1891E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1901	16-1901	TCGCACTCTACCTCTTACCTG	16-1901	CAGGCTGGGAGATCTGGG	16-1901E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1911	16-1911	TCGCACTCTACCTCTTACCTG	16-1911	CAGGCTGGGAGATCTGGG	16-1911E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1921	16-1921	TCGCACTCTACCTCTTACCTG	16-1921	CAGGCTGGGAGATCTGGG	16-1921E	TGGCATGCTCTGACAGGCTCTGCTTTC			
16-1931	16-1931	TCGCACTCTACCTCTTACCTG	16-1931	CAGGCTGGGAGATCTGGG	16-1931E	TGGCATGCTCTGACAGGCTCTGCTTTC			

Table 11

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Table 11



Table II

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')
22-008L	22-008L	CCCCAGGCTGACTACAGAGTGT		22-008R	GAAGCTCTCTAGACACTGG		22-008E	GGCTGGTGGGTTTGTGACTAGGGA
22-015L	22-015L	TGGAACTTATATACACTTC		22-015R	TGTCTGGCCAAAACATACATCAT		22-015E	GATTTCTGTCTGGGATCTCAGATCCAG
22-016L	22-016L	CCAAATGTACAGGTCCTGGCAC		22-016R	CAAGCTATGACCTTAAGATTATG		22-016E	TCCAAGATAGAGCCAGAGTCTCATG
22-018L	22-018L	TCACTGATGCTATGCTGGTTC		22-018R	GTTCAGCTGTCTTACCCCTTA		22-018E	CATTAAGAAATTTGTCACAGTGAAGAAG
22-019L	22-019L	GTCCAGGAGCTCTCTCTACACAG		22-019R	GAGGCGCTCTTCTTCCCTGGCA		22-019E	GTACACCTTCCAGAGTTGGGAACTCG
22-020L	22-020L	TCAAGTGTATCTCTCTGCTCAAC		22-020R	GGGCTGACATATGCAATTC		22-020E	AGATCTCTATATCAGGTCAAGTCTCTG
22-021L	22-021L	GAATCCAACTCTCTCTCTATCT		22-021R	AGCAGTATGCAATGAGCAGTAT		22-021E	AGATGAGAACCCAGCTAACGCCCAAG
22-022L	22-022L	GTCCAGGAGAGTCTCAACAC		22-022R	TGTTTCTCTGGAAAGTGG		22-022E	CTCAACACAGGAATGGAACTACAAATC
22-024L	22-024L	GGAGAGGATGCGGCAAGATTA		22-024R	AGGCAGTGTCTCCAGTCTTAT		22-024E	TTCATTTTCAAAATGTGAGCAAACTA
22-025L	22-025L	CAATCTTTCTTTCTTTTCAACA		22-025R	GTATCTCCACCTTCCAGCTTCTC		22-025E	ACATCTGTCTTCCGACACACTCTGACTA
22-026L	22-026L	TATGTGTAGGCTGTACCTTGT		22-026R	GAATGCCATATACCTCTCA		22-026E	CTCTAGCTAGCTCTCTCTTCCATTAGA
22-027L	22-027L	AGAGCTTTGCTATGTGGCAGTAG		22-027R	GATTTGAGAACTCTGAGTTCAG		22-027E	AGACTCTCTCTAGATCAAAATTTATGCG
22-028L	22-028L	GAATAGGCTAACTGTACTCTT		22-028R	CAGTTACCAAGTATGGCAGTA		22-028E	CTTCACTACCATGTATCTCTCATGGGCA
22-029L	22-029L	CGGGTCTTCCATGTGTGCT		22-029R	GGGGTACAGTATTAAGACTTA		22-029E	TCCAAGCACTCCGCGTGGCAAG
22-030L	22-030L	TGGCTGAGTTAGATGTGTAGCAT		22-030R	ACCAACCGACCTCCGACCG		22-030E	GGGAGCTGTGTCTCTCTGCGCT
22-031L	22-031L	CTGCTCTCCCAAGACTCA		22-031R	AGGAGCTGCTCCAGAGGGA		22-031E	AGCCACACAAAGACTCTCTCTCAGGGA
22-032L	22-032L	CATGGCAGAAATCAGCACTT		22-032R	CCTAGTCTGAGCGGATCAG		22-032E	GTCTACTGACCTACAGAACCATATGGG
22-033L	22-033L	CTGGAGATAAGCTCAGATTTAT		22-033R	GGACAGCAATTCGTGTAAACA		22-033E	TATGACTTACATGTATCTCAGTACGACAT
22-034L	22-034L	TATGATGTCTCTCTCTCACTCAG		22-034R	CCTCAAGGCGCTTACATTTAA		22-034E	TCTCAACTAGTATCTCAGTACGACAT
22-036L	22-036L	GTATGGGTGTGTGGAGTTGACAA		22-036R	TGCGCTCTGTGTCTCACT		22-036E	ACACTCATGTACCGCTTGTATCTCCA
22-037L	22-037L	CAAGATATAGAGGACGTCTTA		22-037R	TTCAGCTGTAAATCTATTGA		22-037E	TGATAAACAAGAGACAGCGCTGTCTC
22-038L	22-038L	AGCAGCCCAATCTACAGATCAATC		22-038R	ACTCTGACCTCTGAAATGTGAT		22-038E	CAAGTGATTAACCTAGCTAGCATGTACAG
22-039L	22-039L	TGGAGAAATGGGACCTTTTAAACA		22-039R	CTCTCGACCAATTCATCTCTT		22-039E	TTTAACTTTCTCAAGAACTGTCTCTC
22-040L	22-040L	TTGGAACTTGGGACCTTTTAAACA		22-040R	GGCTCAATATTAATTCCTGAAAT		22-040E	CATTAAGCTCAAAATGGTGTCTCTC
22-041L	22-041L	CAGCCCTGACTGCAACTCTC		22-041R	CCCAAGGCAACCTGCGTTA		22-041E	ATGCTCACAAAGCTGTGTAGGGCTCTC
22-042L	22-042L	CCCAATTAACCTATGAATAG		22-042R	GCTTCCATGCTCTGGGCAAT		22-042E	GAACCTGAAGCTACAGAAATTAAGACAA
22-043L	22-043L	AGGGCTTTGGCAGCTGTGTAGGAG		22-043R	CCCTGACCAATTTGAGCCTCT		22-043E	GTTCAGATGTGCGCAAGATTCACAGACAT
22-044L	22-044L	GGGGGAGGAGGAGCACTGCTC		22-044R	ACTGAGCTCTGTGAGCCTCAATG		22-044E	TCTGAGCACTGCTCTCAGCAGCAT
22-045L	22-045L	TCCTGAGCACTTTAAACATCTT		22-045R	GAACAGGATCCACAGCAGCTCT		22-045E	GGCTGTGAGGCTGGAAGCCACTG
22-046L	22-046L	TTTAACTGCTTACATTTTGGGTTA		22-046R	CTTCAAGGAATATTTCCGCTTA		22-046E	TCCGCTTACCACTCTTCAATTAACAATG
22-047L	22-047L	AGGTGTGCTGTACCTCAAGCG		22-047R	AGAGCTGTGTAGCAAGCAAGG		22-047E	TGACCCAGAGGCGGCACTCTG
22-048L	22-048L	TGGAAGGACAGTCCAGTGA		22-048R	AAGAGCCAGAAATCTGCCCCAC		22-048E	GTCCAGTGAAGAGACAGCATGTGAACAA
22-049L	22-049L	CCCTGCCACTTACTTGGCATAATG		22-049R	AGTCTCAAAATATCTCTATGTGT		22-049E	ATATGACTTTGGGCAAGAGTGAACCCC
22-050L	22-050L	TTTCAATTTCAATATCCCTTTCTA		22-050R	ACAGAAATTAATCTCTGAAACC		22-050E	TAAAGTGTGAAAGAGCTGGGAACAC
22-051L	22-051L	TOAATTAAGACTTGAACCTTGA		22-051R	TCCTTTCTGCTCTCTCTAGT		22-051E	CTTGAGACTCACAATAAATCTGATGCT
22-052L	22-052L	CATGACAGAGACAGCTCT		22-052R	TCCTTTCTGCTCTCTCTAGT		22-052E	AGATAGCCGAGCTTATGGAAGAACTGC
22-053L	22-053L	GGTGGCCAGGCGGCAAGAGATG		22-053R	CTTTTCTGCTCTCTCTAGT		22-053E	GGAAGGCGGAGCCAGGCTCTCTGCT
22-054L	22-054L	GAAGCAGCCAGCAGATCAGGACAG		22-054R	GGCTTGTATCATCGGCTCTGG		22-054E	CATGGAAGCTGCTCAGTCTCGGAGCC
22-055L	22-055L	CTTGCCACATGCTTGGATG		22-055R	CAGTATGGGAGGCAAGGAAAAA		22-055E	GTTCACAGACTCTGCTGTGTAAGACAA
22-056L	22-056L	AOTGGTGTGATCATAGCTCA		22-056R	TGAGCAGGAGTGTGCTGATG		22-056E	GTACACATATAGTCTCAGCAGCTCAGGAG
22-057L	22-057L	GACTGGATGGGCAAGAGTACGGG		22-057R	CCCTGGGCTCTCAGCGGCACT		22-057E	CGGAGCTCTGCTGCTCAGCTCTCT
22-058L	22-058L	TGCAAGAGACAAATAAGCTACGTAT		22-058R	GACAAACATTTGAGGAAATA		22-058E	GAAAGGTGCTATGAGAACATGGAATGTGGA
22-059L	22-059L	GTGAATGAGATGAGACATAG		22-059R	AGAGCACTCTGAAAGATAATG		22-059E	TCTGTTGTGCTCTGTTGCTGCACTGATAC
22-060L	22-060L	AAGGCTGAGAGAACTAGAGAGCC		22-060R	AAATCCCACTCTGTGAAATACAG		22-060E	TTCGAGCTTTGATGCGCAGCTACTCTG
22-061L	22-061L	TGGCTCAGTTGCTCTCTGA		22-061R	ATGCTGGAAGATGCCAGGTGCTCA		22-061E	GGTCCAGCTGAGGAGGTTTGTGTGCG
22-062L	22-062L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-062R	GGCTCCGACCTGACCACTCTCC		22-062E	GGCTCCGACCTGACCACTCTCC
22-063L	22-063L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-063R	GGCTCCGACCTGACCACTCTCC		22-063E	GGCTCCGACCTGACCACTCTCC
22-064L	22-064L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-064R	GGCTCCGACCTGACCACTCTCC		22-064E	GGCTCCGACCTGACCACTCTCC
22-065L	22-065L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-065R	GGCTCCGACCTGACCACTCTCC		22-065E	GGCTCCGACCTGACCACTCTCC
22-066L	22-066L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-066R	GGCTCCGACCTGACCACTCTCC		22-066E	GGCTCCGACCTGACCACTCTCC
22-067L	22-067L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-067R	GGCTCCGACCTGACCACTCTCC		22-067E	GGCTCCGACCTGACCACTCTCC
22-068L	22-068L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-068R	GGCTCCGACCTGACCACTCTCC		22-068E	GGCTCCGACCTGACCACTCTCC
22-069L	22-069L	TCCTCAGTGTGAGTATCCCAAGACAAATC		22-069R	GGCTCCGACCTGACCACTCTCC		22-069E	GGCTCCGACCTGACCACTCTCC

Table III 627 single nucleotide polymorphism (SNP) markers

Note: In each block: First part of the first line, Name of the SNP; Second part of first line sequences length shown; G/A or alike, polymorphic site showing nucleotide sequences variation; Other parts, nucleotide sequences flanking the polymorphic site.

01T002 132bp  
CACGTGTGAG GCCTTGGTCC CCACCTGTGG ACTCAGGGTC TCTTTCAC  
G/A  
GACTGCGGGG AAGGCAGTGG GAGCAGCAGG AATGGATGGT GAAAGGACAC AGTGCCCGCC  
CCCCGAGTGT CCGAGGGTAG AGC

01T003 145bp  
CTATAGCCCC TCTGAATGGT CTGTGACACA TGCATGCTTT CAGCTATTCT CTCTATAGCC  
CTTCTGAAC  
A/G  
GTCTGTGACA CCATTATGCT TTCAGCTACA GTTTGCTTTC TCTGGTTTTT CAGTGGTGCT  
CTGGGGAAGG CAGAA

01T006 141bp  
AAAGAAGAGA GGTTTTTGGG GATATTTTTA ACACATCTAT AATCTTTCAT TAACAGCTAG  
AAATTTAGAT TGC  
C/T  
GTACATAAGT GATAGACAAT GAAACAGAGA AGGCATTTCT GAGAGTCTCT CGGCTGTCAG  
CATTGTG

01T008 147bp  
ACTAAGGAGG CATCAACAAC TCTCCCAGCA GCTGATGGAG GATGGAAACC ACACAAGTGC  
GGAGATTCA GGTGGGGACT TGGTGGGGGT CGTGTGAGCC  
C/T  
AGGGAGAGAG GACGGAAATT CAGCAAGGAC GTAGAAGAGA GTGCTT

01T009 130  
GTACGGTGCT ACAGGACCCA ACAGAGCCAG AGACTTGACC CAGGTC  
A/G  
TTTAGCCACC CAGCCCCAAG CCAGCAGGGC CAGCCAATGG GAGCCTGTGT CCCACCTCTC  
GCCCCCACTC AGACTGTGCT CCC

01T012 138bp  
CAACTTGAAG TAGTAGGTAT TGGAAC TAAG AATGATATAA ATAGAAATTA ACAATTC  
G/A  
GAGATTAGAA TAAGGTGCAG GAAATTACTC TGCAGTGTA TTTTGTGTTT CTCTTAATTC  
AAGAGAGCTT GGAATGCTA

01T013 131bp  
GAAATTCTAT CTCACCACCG TGAACTCTT CAGTTTCTA ATTGCTTTAT CAGCAGGGGG  
TATAAAGGT  
C/T  
ATGAAAGCAA TTTCCACATG CTGTGGCTCC AGGTCTCTGG GTGTGAAGCA GAGCAAGCCT

01T014 140bp  
ACAGCCTGTC ACAGAAGTCC TCTTTGGACC AGATAGGGCT GCCTCACAGG GGTTCAGTT  
TGTCATTTC  
A/G

TTCAACAAGT CCTGAACACT TACTCTGTGC CAGGAATTTT GCTGGGCATT AGGGATCCAG  
AGAAGAAGA

01T019 139bp  
ACTGGCCACC TCTGCAGAAG CTAATTGTCC AGAGGAGGGA AAATACAAGT TTATAAATAA  
CTAAATATC AGGTCAAGCA CATTGCAGG  
A/G  
AGCAAAAGTG GAATAGAATA ATGGGGCTGG GAGCTCCAGG AGGAAGAAC

01T020 147bp  
AACACCTTGC CTGGCATATA GTAGATACTC AATAAAATCT CTGTTGGATG ACTGAGTTTA  
GGCTGAGGGA GAGGGAGAAG AGGGAGGCAG GGAA  
G/A  
CAGGAATGTC TGGGTCCTTC TTAGGCTCTC ATTTGAGTGT CCTCATCCAT TC

01T023 131bp  
AGATTTTCTT GACCGTCTTC TTATTCAGAA TTCATCTTAA ATAAATGTCA CCTCCTCAGA AT  
A/G  
GTCCTCCTTG ATTGCACTGG CCAAAGCGGC CACTCTGCTC CCCAAGTCAC CGTTGAATCT  
ATCCTTTT

01T025 138bp  
AAGGGATAAA CCTCACTGAC TTGGAGGAAA TCAAGAGGAG TGAGCACAGC ATCAGAAAGC  
CCCCTGGCCC CAGACTGCAC CC  
G/A  
CTTTCCTGGC CCTACCTTGA AATCCATCAG GTCTGCGTTG GACACGGCAT TGTAC

01T028 146bp  
CCCAGCGGGA AGCTGTTGAA ATAGTTCAGG GGAGACGGGA GAGGTTCTGG ACCAGGGCAG  
GGCAAGGGCA GAGGGGAGGG TT  
C/T  
AGGACCTGGA GCTCAGGTGG TGCTGATGGA GCAGAGAAGG GAGACAGACC CGCATGTGCT  
TTC

01T029 108bp  
AATTTAGGCC TTTATGTAAA TTCAGAATGA TACAGATTTA GACTTTATAT AAATTGCCA  
A/G  
TAAGTGGCAG AGTCAGGTCT TGAACCCAGC TGCTCTGAAT TTAAAAGCCT TTGCCCTC

01T032 101bp  
CAAAAGACCT CCAAGTCTTA AAAAAAAGA CCTCAAAGGC CTAAATCTGT TCAAAGCTTC  
A/G  
AGGTATTTCGG CAAGGATCTC CTAAACTCTT TTTTGTCTT GGTGGTATGA

01T035 RsaI  
GTGCTCATGA GCCGCACGGG GCCAGCGCTG GTCCTGGGAC GGGT  
A/G  
CGGCCACCGG GGGCGCTGCT CAGCGTGCCC GTGCTCAGCA GCCT

01T037 122bp  
CCATCAGGTA ACTGACAAAC TCTAAGGAAG CATCTCTGTT TTTCTGGCCC TGTACTAGGT  
TCTGGAAGG  
C/T  
GGTGAGCCAG CAGGCAGGCC TGGGACTGGG AAGCCAGCAC TAGGGCTCAG GG

01T038 130bp  
TCTTAGCAGG GGAACAGCC TAGGCAAAGG CCTAGAGGCT GGAA

Table III

A/G

GGGGTAGGTT TGTATGAGCC ATGGTGAACC AAAGTGTGAG AAAGAAATGG CAGGAGAGGT  
TTGAGTCCGT TAAGAGAAGC CTTGA

01T039 130bp

CTCTCTAGTA AACCCGATCA CCTCCCACTG GCATGTGCCT AACACGTAGG AAGTTCTCAC

A/G

ATGCCCTATT GTTAATGATG GATGACTCTA ACTATGATAG CTAATATTTA TTGAAGGCTC  
TGAGAAGCC

01T041 149bp

TCTCCAGTGA GTCTGGGGGC TGGCAGGGTG ATAACACGAG GCCAAGGCTC AGAGAACTGG  
GCCCTGGTTC CTAGGCCTGG CT

C/T

TGACATTAAA AGCAGTATGA TCTTTGTTTG ACAAGTTATT TCACTTCTCC AGTCTTCAGT  
TTCCAC

01T042 127bp

CTCACTCCCT CAGGCCTCCG CCCAGTGCTC TTTCCACAG AGGC

C/T

TACCCTGACC ACTTGATCCC AAACAGCCCC TGCCTGTCCT CCCTTCTCCC TCCCATCCAT  
CTGTTCCCTGC ATCATCTTCC TT

01T043 113bp

ATTCTCGAAC TTTCACGCAC AGAAGAATCA CCCAGAGGGC TTGTGAAAAC ACAGA

T/C

TGCTGGGCCC CAGGCCCAGA GCTTCTGATC AGTAGGTCTG GCCTAGGGCC TGAGAAT

01T046

TCTGAACACC CGGTTTATAG TCCCAGTCCT GCCACTGTAG GACATTGAAT AGGTGATGTT  
ACTCATCTGA AATTGTATCT

A/G

TTTTGATAAC ATGGGGATAA TATCTCTTCT CTCTACTTGA ACAATGAGGT AACACTGATG  
ACC

01T047 147bp

CAGAGGGGTT GCCGTTGCTC CTTATCCTCC CATCATTTGA TAATGTCAGT TTTTTTTTAA  
ATTTTAACCA TTCTAATAGG CATGTGGTAG TATCTCACTG

C/T

GGTTTTTATT CATGTTTTTC TAATAACTAA AGATGTCGAG TGCCTT

01T048 140bp

CCACACCCTA GAAGGCTGTA GAACATGAGG ACATGAGCCA TGTAGGACGT GAGGATGA

T/C

GCCAGGGTTC CAGTGCAAGC TGAGACTTAA GGGTACCTTC CAAGAAACCA GGAGGAAAGA  
GCGCAAGGAA CTGGAGTTTT T

01T051 130bp

CTACCCTGCC TCTGGGCCTT GACCTGTGCC CTCTTCTTCC ACAGCTGTGA TTGTGGGCGG  
GGTGGTGGG

C/T

GCCCTCTTTG CTGCCTTCTT GGTCACACTG CTCATCTATC GTATGAAGAA AAAGGATGAG

01T054 133bp

TGAGATGGCC CAGACTCCGT GCAAAGGAAG GCAGGATGAG GAGGAAGTGA CC

A/G

TCTTCGTCAA GGTGCACAGA GCTGCACAGC AGCCCAGATG GCTCTGCTGA GAAGACACCT

Table III



CATTTGGAAG TAAACACAGGC

01T055 118bp  
CCTGGGGCCG GTGACAGGAA AACTAGACCT GAAAGTGTGA GAGGAAAGAG AAGTTGCTTG  
AACTCAGAGA G  
A/G  
CCTCTGTGGA GAGGGCCATC CTGCAGGAGC TGAGATCTTC CACTAA

01T056 122bp  
CACAATGGGA ACAATAAATC CAACCAGAAG GAGGGCCATG TGTGTGAGCT TGACAGTGCA  
A  
T/C  
GCATGGGAAA AGGAAGAGGG CGGGTCTTCC TGGGTACCA ATTCACATCC ACCACCATTC

01T057 137bp  
CCCATTAGCC AATGAACAGC TTGTTTCTCT TCCTGAAAAA AGGATAGATC TTACA  
C/T  
TCCCAAAGAA TCAGAGCCAG ATAACAGCAA CAACTTATT GATCAGTTAC TATATGGTAG  
CCATAGTTTT GTGGGTTTTT T

01T058 142bp  
GTGTTCCCGG TCGGCATATG ATGAAAAACA TGGGTTTGT CTGGGCTAG GTCTCGGTCC  
GAAGCATGAA GGGATTA  
C/T  
TAAACCCCTC CCAATTACTA TAAAATAAGA CAGTAATGGT TTAGATTATC CTTTTTAGTG  
GTGG

01T060 130bp  
GGACTGCTAC TACACAATGG AGGTAAGGAA GATTATGTCT GGAATAAAGA AGATCC  
C/T  
TTAGGTTATC TCTTAGTATT ATCATGGCCT ATGATTAAGA TCAATGAAAA ACCAGAACAA  
CTCAATCCAG GCA

01T061 125bp  
CCAGCGTTCT GCAAGGGGCT GGGTAGAAGG GGCTGGCATG GGCATCTGGA ATCCTTCAGC  
CTAGTCCTCT GGC  
T/C  
CGGTGATGAA AGCCCAACCA CTGTTCTCAG ACCAGCAGGG ATAGTCTATC C

01T062 142bp  
AAATGTGGTA CATGGTCTTT GTAGTGATGC CTGTTTTTCA AAATTTCACT CTACAAACAA  
CCTCACCA  
T/C  
GAACTGTTGT GAGAACTGTG GGAGCTATTG CTATAGTAGC TCTGGTCCTT GCCAATCCCA  
GAAGGTTTTT AGT

01T063 95bp  
ATTCATCACA TAAAATGCAA CTACCCTGTA ACTCACATAT GTAAAT  
C/T  
CAATAGCAAG AACATTCTG AGATTCAGCA GTGGGATTTT AGAAAGCT

01T064 146bp  
GTGGTCCTAC ACAAAGAAAC GAATATTGGA AATGGCATTT AGAAAGCATG TACTACACGT  
TTTCTTATAA TTAAATCTT TCAAAAAATA TTTGACGTAA  
T/C  
AAATAAAAGT AATAATAATG AATCACAAAG GTTATAGTGC ATAAA

Table III

01T065 141bp  
 GCCACTCCTG ATGGATGATC TTACTTGCTT TGCCAATGAC AGGAGTGAGA TGACCCATTT  
 CTAGCAAAGC CATGAGGCCG TATCTG  
 T/C  
 TGGAGCTTCC AGGGGAAGAC TTCCTTGCTT TAGAAGGACA CAGAAAAATC TGTC

01T066 148bp  
 TTGAAAGTTC TGGTGTATAG CCCAAAGGGG ACAGACAAGA AACTTAAGAG TCTG  
 A/G  
 AAGGGGTAAC AGGGGCTTAC GTACTTCTGT TTCTTTGATC CTTTATGAGT TTTCTCTGTT  
 TTTTCAGCTG ACCTTTCCTT TGAGTGACTG GAG

01T067 143bp  
 AGAGGGATAC TTGTAAACTG AAAAGGCTGA GCCCAGAAGA TAATACACCA ACCAACCTCT  
 TTCTTA  
 C/T  
 CATTTCTAGG CCCAGTGTT ATCTGACTAT TCACCTAAAA TTGTAGAGAC TCGAAGGGTT  
 GTGGCAAGAA CACTGG

01T068 125bp  
 TACAATGCTT TTCTTCAACA ATAAACAGCA AGATCAACAC ATGTACT  
 A/G  
 GTATAGCTGC TTAGCATTTT TAAGGGAAGA ATAAATTATA TGGCCAGCCA GCTAGCAAAA  
 TAGAGTGAGC TACCACA

01T069 131bp  
 TATCCCTCCT GCCATCCGTG GAAAAATTGT CTTCCACGAA ACTGATCCCT GGTGCCA  
 G/A  
 AAAGGTTGGG GACCACTGTC TTAAAGCATG CCCATAAGGG TGGGTAGCTC ACTGGACATC  
 TACTGAACAA TTT

01T070 131bp  
 TTGTCTCCTC AGGTAGTGAT GAATTAGTTG CTGTCACAAA AGGAGGGAAG TAGCACCCAA ATTAA  
 A/G  
 TTGCTTAAGA GAGGAAATGT ACATCTTGTA TAACTTAGGG AGCGAAGAAA ATGTAGGCGC  
 GAAAG

01T071 141bp  
 GGCCCCATT CCAAGAACCA CGCTGGGCCA GGTACATGG CTCCCTTGGA GCTTTGATGG  
 CACTTC  
 T/C  
 TTGGGAAACA GAAGCTGAAT GTTTAAGAAG CATCTGTCAT TATGGAAACG AAGTTGCCAG  
 GCCATTTTTT CTTT

01T072 146bp  
 TTGTTCTGTTA TGTATCACTT CTTTAAAACC TCAAAGGCAG GTTGATCAGT AACCAGGAAG  
 AATGGATCTT TGAATTTCTG AATTCTTG  
 T/C  
 AGTAAACTT TCCGATGTCA TCCAAATCCC ACCCGAATTT CTTTTTAATT GAAAGA

01T074 102bp  
 ATTAGCACGT CAGCTTCTC TTGTGGTATT TATGTGTTTA TATAACA  
 T/C  
 AGTTCATTGT TCCCAAATGT TAGTCAACTC CAACTATAAA TCAAGCCCCA AATC

01T077 124bp

Table III

CAAGAGAGGT CCCACCAGGA AATATTATAG TCAAACGTG AAAGGCCAAA GGCAAAGAGA  
AAATCTTG

A/G

AAACAGCAAG GAAGAAGCAA CTGTTTACAT ACAAGAGATT CTGAATAAGA TTGTC

01T079 127bp

GATGGGAGCC AAACATCATC CTTTTATCAG GAACCCACTC CTGTGATAAC TAACCTACTC  
TCATGATAAT GACGGCAGG

A/G

CCCTCATGAC CTAATCACCT CTTAAAGGTC CTGACTGTCA ATGCTGT

01T083 129bp

CCTCTTATCT GAGAATGACC CTTCTCCCC AAGGAGTCCC AAAAGGTGGG CTTCTTTGTT  
GATTTAGAGA

A/G

TCGATAATTC AGTAAAGTCC CAAGTAAATG GCACAACACA AGCTCAGA

01T084 142bp

CAAAGGGACA AATACTGTAT GATTCTACTT ATATGAGGTA CTAGAGTAGT CAAATTCA  
C/T

AGAGACAGAA AGTAGAATGG TGGCTGCCAG AGCTGGGGAA TGGGGAAATG AGGAATTAAA  
GTTTAATTGG CAAGGAGTTT CAG

01T087 137bp

GCTTCAGAGC TCTGCCAGCT GCCATTCTAC AGAGGCAAGC CCCTCCGGCC CCATCTGGCC  
TCCCTGACCC AGGG

C/T

GCTGGCCTCT GATTGCATTC CCCTAGTGAC AGGGAGCTCA TTAGGGCCTG GGGCTTTGGG  
GA

01T088 145bp

CAACCCCAAG ACTCCCAGGC ACATGGGATG GATGTCCAGT GCTACCACCC AAGCCCCCTC CTT  
C/T

TTTGTGTGGA ATCTGCAATA GTGGGCTGAC TCCCTCCAGC CCCATGCCGG CCCTACCCGC  
CCTTGAAGTA TAGCCAGCCA A

01T089 146bp

ATTTACATGC ATTTAATCCA CGCAGCAAAA TCCTAGGAAG ACAGTATTAT AGACCCTATT  
TTGCAGTGAG TAGACTGAGA CCTAGAGAGG C

C/T

GAGCCACTTG TTCAAGGGCA TACAACCTACC TGGTGGGGGA ACAGGACTGG AAAC

01T090 147bp

CAGCATGTTA TAAATGCTAT ATGGAGTAAT AAGTATGGTA AGAGAATAAT GATTGAGGGT TGGG  
A/G

TTACAATTTT AAATTGTGTG GTCAGGAAAG GTGACATTTG AGCAGAGACT TCAGTGAAGT  
GGGTAAGTGA ACCATGTGGA TC

01T091 147bp

ATTTGGAGCC ATAAACATA TCTAACTAA TTTAAAAGAA TGGAATTCAT ATAATGTTTA  
CTCTCTGGCC ACAA

C/T

GGAATGAAAC TAAAAATAAG TAACAAAAAG TTACCCAGAA AATCCCCAAA TACTTGCAGA  
TTAAACAACA CA

01T094 112bp

TCGAATCTCG CCCAAAGTGA CGAATAAATC CGGACTCTCA GCAACATGGG CTATAGGGAG GATCC

Table III

- 6 -

C/T  
TAAGAATTCC TCAGTGACCA GATAACTCTG TGCATAGACC AAGGTA

01T096 116bp  
TCAGTGCCAG AAAGATGTGG CTTAAGTTCC TGCGACTCCC TTAATGTGGA GCTCAGACAC T  
T/C  
GCCATGGGGA GAGCCAAACT GCCTTCACAG CACTAGATGC TCCATAAGGG ACCA

01T097 148bp  
CAGGGTCCCT TTCCGTAGAG CCGCCAAGTT CTGGTTCCTT GTGGGTCCCG C  
C/T  
ATGCACCTTC CATCCATATG TGCACATACC AATGTGCAGC TCTTTTTATT CATGTAGTGG  
ATTCCGATCA CACATATAAT ATGCCTGTGA CGACTT

01T098 134bp  
GGCCAAGGTA TAATCACACT GGTAGCTGGA AAGCCTTCTG GGCTGGGGTG CCATAGGCTG  
T  
A/G  
TTTGGGTTCC AGTTCCAGCG CTGACTTTGC TCTATGATTC TGGACAAGTC ATCGCCCTCT  
CTGGGCCTCA GT

01T099 145bp  
CCATTGCTGT GTCCAGGGC ATTTGGCAGC ACGGCTGGGT GGTTGAC  
A/G  
AGGCCAGGAG TAGTATGTGC AGGCACAGGG TGGGCGTGGC AGCTGTCACA TGGCAGAGGA  
CCCGCAGAAG CTGCTGATGG CTGGAAGGTA ATTAACA

01T102 130bp  
AAGAAGCCAG GTACCAAAGA GTACATACTA TGTGAATCCT CTTAACATGG AATTCTAGAG  
CAGGCATAAT GGTTCATAGT AC  
A/G  
TAAAGCAGAC CAGCGGTTGC CTAGGGTGAG GAGTAGGTGA TGGGAGG

01T103 148bp  
GACAGGGTGA TCAGGACAGC TTCTATAAGA AGGTGAGGTA TGAATTAATG C  
C/T  
TAAAGGAGGG GTGAACATGA GCTAGGCCAA TTGCAGGAAG AAAGGGTCAC CAATGAAAAA  
GCACAAGCTA GGATACATCC CAGGAAAGAG CCAGAT

01T104 109bp  
CTGGGAAGAC GTCTCTTCAA AGCTATTTGA AAGAACTGTG CTTTA  
A/G  
GAGATAAAAT ACCTAAACAA GCAAATCCTC AATTTCTTTA CACAGACTTT CTGTCATTAG  
TGT

01T105 140bp  
AAATGTCTGC AGTCTGGCCT CTGTCCCCTT GATGCCAAAC AAAAC  
C/T  
GCCCTGCCCA AGGTCACCTG TGTAATCTA AATGACACCC CTCAGCAGCA GTGGGAGCAT  
TCTGTCTCTG TGTGTTCTCT GACTCTGTGG CCTC

01T108 134bp  
GGATGAGAAG GAAACAAGCC TGGTGAAATG GAATGGTCAG AAAAGCCTCT  
C/T  
TAGCATAGTA CTAATTACGG GGTAAATTTT ATGAGGAGCC TGATTTGGAA GTTCAAAAGA  
GGCGAGAAAC TAGACAGAAT GAA

Table III

01T109 107bp  
 CATTGTGTG CTTGTCTCCC TCAAGAATAG GGACTTCTCA AAAATCAAGC TACATGCTGC  
 AAGTGCTTGT ACC  
 C/T  
 AGAGCTCTGA ATCTGACACA AAGTAAGGTT CATACGCATT CAA

01T111 122bp  
 GGCTTATTTG ATGGAAATGG TAATAATGAT AATAATAACC ATGAACCTAC TGAATATGAA  
 ATATATTAAT AA  
 A/G  
 CCATCTTAAA ATGTTATTTA CTCTTCACAA CAATGAGAAA AATGTGTAT

01T117 144bp  
 GTCTCCATCT CTCTTAAAGG AAAAAAAGAC GACATTACAC AGCAACATGA TTATTTAATT  
 AATAGCTTTT CC  
 C/T  
 TTTGATGCCA GTCTTGTTTT AGTTATAATA AACTAATAG GTATATCTGT CAAAGGACTT  
 ACAAATAAAA G

01T118 126bp  
 TGCCAATCTT TCTGGCAAAA TCAAAAATGC TTCCAAACCC AGGGAAGCAG  
 T/C  
 ACTACTCTGT GTGAGAAGTT CTGTATAAGC ATAGCTATCC CTAAATGCAG GCTAGCAACC  
 ATCTCCCATC ATAAA

01T119 143bp  
 GCCAGAGGCT GATGGCAGTG AACAAAACAG ATGAGTTATA GCTTTAC  
 C/T  
 AGTTGGTGAA AAAGAGAGTT TTTAAATAAA AAGTTATACA ACTAGATATA ATTATAAATC  
 ATGTTTACAG AGTTATGTGT GAGAATTAAA AGGGA

01T120 142bp  
 CCTATAATCC CAATGCTTTG GGAGGCAGAG GTGGGAGGAT TGCTTGAGGG CAGGATTTCA  
 AGACCAGCCT GGGCAATATA GCAAGACCCC ATTTT  
 C/T  
 ATAAAAAATT TAAAAAATTA GCCAAGAGTG GTGGCAGGCT CCTGTA

01T121 120bp  
 GAGGCAGGGT AAGCAGGATT CAGATTGGCG AGTTGGAATA CTTTCAGCAG GCTCAGGGCT  
 GGCTGTCTTT AGTTGTC  
 C/T  
 GGTACCTGGG CCTGGGGTGA TTAGAGGCGG GGAATACTGG CC

01T127 140bp  
 GGAGCTGCCC AGAAACAGCC TTGTGGGGTG GGGTTGGTGT CTGACCT  
 T/C  
 CCTCCCCGGG GGCCTTCGCA GGCTTCTCTG CTGGTGCTTC TGTGCCTGTG GGTCTGGATT  
 CCTCCAGGGC CTGATCCTGG GTGCAGATGC AG

01T128 142bp  
 TCCCAGGGGC TTCTGTGGCC TGCTGAGGCG CAGTGGGGGA GGCTGGCAGA GGCAAGAGGG  
 CAGGGCCTGA GGGATGG  
 A/G  
 GATGGGAGGC TCTGCCTCTC ACATGTCCTG TCCTCTCCAG ACCCCAGGGC TCCGTCCTCT  
 GGAC

01T129 141bp

Table III

ACCCAATATG CCAGTTAATA CTGACATTTC CAGTGGGAAG GGAAGAGGTG AGAAGATAAC  
ACCTGAGTGG GCTGATGAGC C

A/G

GAACAGTTTA AGTGGGGGAA AGGTCTGGCA TTGCCTTAGA GCTGGTGACC AGACTCCCC

01T131 133bp

CCTGTTATTT TCCAGAATAA TCAGTGATAC TCTGTGATAT TGATAATCTA CCTTGTGGC  
CCTTACCAA

A/G

TTACTGGGTG TGAGTAACAG CTGACTGTAG CTCCTTTCT CTACCCTAGT GCTCTGGAAG  
GAG

01T133 126bp

AATCTACCAA TCTGACAAAG GGCTAACATC CAGAATCTAC AAAGAACTTA AACAAATTTA  
CAAGAAAAA ACAACAA

T/C

CCCATCAAAA AGTGGGCAAA CAATATGAAC AGACACTTCT CAAAAGA

01T135 129bp

TTAAAGTCTT TTATGCCTTC CCACCCATCA TTAAAAATTA ATAAATTTTG TCACTCAGCC  
ATTTACAAAA TAATCTGATA

C/T

TACAGATTAT TTTATTTCTT TCTACAAGAA AACCATATCC TATTTCTT

01T137 148bp

AAAAAGGAAA CCACCCTTCT ACCAGGGACC CTTAGATCGA CCCCAGGAGG AGCCCTAGAT  
GCTGTTCCC

A/G

TACCACGCCC TCTCCAGCGG GAAGTAGCCA GAAGAAGTTG TTGCCCAATT CCCCCTAACA  
GCAGTTAGGG ATTCCATT

01T138 105bp

GAAATGATTC ACACCAATTC ATGATAGAAG GTTGCACTTG C

A/G

GAGGGTTGGT GTATTAGTCC ATTCTCACAC TGCTACAAAG ATACTACCTG AGACTGGGTA ATT

01T145 149bp

GGCAGCTGGA GGTTAAGCAT CTAAGATTAA TTCCTGAACA CCAACATAGA AAGGCCAC

C/T

AAGGGAGTTG CTGCCTGTCT GATCAGGAAG CTTCTGGAGT CAGGAGCTGC TTCTTTAGTT  
CCTGGTTCCA GGATCATCCC AGCTCTGCTG

01T146 127bp

ATGTGTTAGC TCCCACTTGT AAGTGAGAAC ATGTGGTATT TGATTTTCTG CTCCTACATT  
AATTGCTTA GGATTATG

A/G

TCTCCAGCTA CGTCCATGTT GCTGCGAAGG ACATGATTCA TTCTTTCT

01T147 140bp

AATATGATGA AGCGTAGTGA AACACATAT GTAAAATGTT ATTTACA

A/G

TGGCAAGTAC TTGAGATACA TTCAGTAATG AAGGCTATCA TCATTGTTAA TGGCAGGAAT  
TTTCAAGTGA GTCATTATGT TTACATGCCA CA

01T148 102bp

AGGAAGGAAT AATAGAGAAA CTTACCCAC TTCTTTGATA AGTAGGACC

G/A

Table III

GACTCCATGA GCCATTGATT ACTTCTTG TG TCAGACTGGC ACATATCAAG GA

01T150 100bp  
TCAGAAGAAT CGTTTGAACC CTGGAGGCAG AGGTTGCAGT GAGCCGAGAC AGC  
A/G  
CCATTACACT CTGGCCTGGG CAACAGAGAG AGACTGACTC AATAAA

01T151 126bp  
GTACATTGGC CCCTTTTATC CATAGCTGGA GTGGCTGGGA CACAGGACAC CAA  
G/A  
TCCCTAGGCT GCACACAACA CAGGGACTGT GGGCCCAGCT GATGAAATCA GTTTCCTCCT  
GGGCCTCTGG GC

01T152 134bp  
TTCTTCTAAC TTCATACTGG CTTGTTTG TG AAAGAAAAGT CTTTGAAAAG GCTACCTG  
C/T  
AGGTGATAAA GATTTTTTAA GTATTCTTTT CTTCTTTTTT ATTAGAGAAA ATCCAAAGGG  
AGTTTTAAAA TTTGT

01T153 141bp  
ACTGGATTAT GCTCCAGGTA TCTGACAGGT TTTCAATACT ACTA  
A/G  
TATGTTTATT ATAGCATAAA AGGGCAATAT AAAAATAATT AAGAACATCA ACTTTATAAT  
AAACAAGACT AGATATTGAA TCCTTGCTCG CACTTC

01T154 117bp  
CCATTCTTCC CGTTAAAATA GCAAATCAA GGATACTAGA ATAATGTATA ATGTGTTCAA  
CACTAAATCG  
C/T  
ACCTTCGAAT TTATATACAG TTTTAAAGAC ACTGACCCTA AGGAGA

01T155 149bp  
GGATAACCTG ATGAAATTCA AACTTCTCTG AGTATCCATT TCCTTATCTG CTTATTCAA  
C/T  
TGACTAGTCA CCTCCTCTCT TTGGATATCT AATAGGTACT TAACATTTAA AATGCCCCAA  
ATTGAGCTCC AGATTATCAC CATTCCCCT

01T156 130bp  
TCCTTCTCCC CTGGTGTTGG GGCTTCTATT GTGAGGTGAC CTCTGGCTG CTCCCTTATG  
GGTCCCAGGA CCTAACCACA GTTG  
A/G  
CCAATCATAA TCCATCAGGC CCAGTTTGTT CAAATGAAT TGCTC

01T157 135bp  
AGCATGTTTCG GATTTCATGA CTCTTGTTGGT TTTGTTCCCTA GACAGGACCT ACCAGGGGAG  
CCTCCTGCAA ATGAG  
G/A  
TGGTCTTCCT TTTCTACTCA TCACATTCTA TGCCTGCCCT CTCTAACCTA CATGGTATA

01T159 139bp  
GTTGAGTCAT TTGGCCTCCT TGATCCTCAC GTAAATTGTG GCATTATTAA AGTT  
C/T  
GGTCTACATC AAATGGTCAT TACAAAAATT CAGTAAGTGT ATAAATATAC TTTTAAACT  
AAAAAGCTCT CAGGAGGCTG AAGT

01T160 147bp  
CCCCTATGTC CCACAAACCT GCCAATCTCA GATTTCTGTAT CTCAGTTAA GATTCCTTCA G  
A/G

Table III

TTTTTAGTTA TTCAGGTTAA ATAATCTTTG ATCTGTATCC TCTATTAAGT CCATCAGAAA  
ATCCTGTTGG CCTTTCAAAA TATAT

01T162 136bp  
AATTAGGTTT GAAAAGGGAA ATAGTAGAAT TAGAGTTGGG TTTAGAAACA AAATTAGTCT  
TGTAATAGTA ACTATGCT  
C/T  
TTCTAGAGTG AGGCAGTATA GTCATGGAGG AGAACTGCCA AGGGATTATT TTAATGA

01T164 122bp  
TTAACTTGTT CACGTAAAGT CCATTCATAT ATTTTGAATA AGGTATAGAG GAGAGTTTTT  
GAGTGACTCC TCACTC  
G/A  
TCTGAAGGTC TGTGACCTAT GAACTGCCTC AAGGCTTTCT CTTCA

01T166 138bp  
CACATTTCTT TTCCATGTGG TATGTGGTGA AAAACAGAGA AACAATAAAA CCCAAGAAGT  
CTTATTATTA TGACTCCCTT CTTAAAATGC C  
C/T  
AAAGAGCTCA AGAATAGTAT CTTGGGAAAA TTACTATGTG TATGGA

01T167 105bp  
ACAAAATTTT AATGCTCTGT GGATCATTAT CTGGCAACAG ACCAACAGCA GA  
G/A  
CATAAACAT TAACAACATA AAGCGGGTTC TGAGTCCTTG GAGTTTCTAA TT

01T169 131bp  
CATACAACCT CCCAAGACTA AACCAGGAAG ATCAAATTCC TTACTAGACC AATAACA  
T/C  
GTTCTGAAAC TGAGACAGTA ATTAACAGCC TACCAACCAG AAAAGTCCAG GACCAGATGG  
ATTTACAGTC AAA

01T171 133bp  
GCAAAGGGTA AGAAGAGGAA GTGGCTTCCC TTAAGTTAGA AGCTGTTTTT ACCTATGGGC TG  
T/C  
GACAATGCAC TGGCCATGTG TTCTAGACCT AATCTGGGTG AGTGAATAAC TGGGAGGATG  
TGGAACCCAG

01T172 148bp  
ACACTCCAGG CCTGATACTT CTGGTGTTAA GCAATTTGCA AAATGATATA CTAATGACCT  
TTCAAAAAGT TATT  
A/G  
CCACATCTGC TCTTTGTCAA GTGCAAGAGC CTAGTATATA GAAAATAATA TTAAGCTCCA  
AGTGAATACA AGA

01T173 148bp  
TTATAGAAGA TCCCCATTGA CGATGCTTTC AAGTTGAAAG AACATTTAGA TAAGCCATTT  
GATATAGAAG TGACTTTTAT TTCACGGTCA AAACAATT  
G/A  
TCAGCCAAAG AAAGTTCCTA ATTTTGTGTA TTTGTGCACC ACAGTAAAT

01T174 140bp  
AGACAGTTCA CTGTATTCTT CCCCCAATTC CTAGAAGAGT AGTAAGGGTC TTAAGGCGGG  
AGAATGAGAC CTCCTGAAAT  
A/G  
CTTATGAAGC CTTCCCTTAT CAAGTACTCA CAGCCAAATA TTTTCAAGTG GCGTTAATT

Table III



01T176 147bp  
 CAGCTGAGGC ATTAATATTC ATTGGATTGG GGGGGTGGTT CCAAGATGGC  
 T/C  
 GAATAGGAAC AGCTCCAGTC TACAGCTCCC AGTGTGAGCG ACGCAGAAGA TGGATGATTT  
 CTGCATTTCC AACTGAGGTA CTGGGTTTCAT CTCACT

01T178 134bp  
 CCTGTTAATA GCCACTACCT TCTTTTCACA TATCACACTT CCGCTTGCTT GTTAACATTC  
 CTCAGTTTTTC ATTTATGG  
 C/T  
 TCAATGAGTC TGTTTTGCTT TACTTTATTT TAATTACTAT AGAATGTACT GGTAACTTTC TGATG

01T180 119bp  
 TACCAGATTT GAGGCTCAAT ATCTACTTCT GAAGCTGGGA GTTGCAATCC  
 C/T  
 TGAGTTCACC ATTTTCTTTC ATCACTTTGT CCAGTGAACCT TAGGACCAAC CAACCAACTT  
 TGTTATGT

01T182 139bp  
 CATGCCTTTG TCAGGAGGCA TTCCCTACGT TCAAGTCTTA AGCATGTGTC CTGTATAAAA  
 TCAGTCTTTA GCGTCTCCCA AAAGAGCTAT CACTT  
 CCT  
 C/T  
 CTTTTATGAA CTTGCTGTAT CTTGTCTCTT CACTTGAGCA CCT

01T184 129bp  
 ACCCAGCCTA GGGCATGGCA CGAAGGAAGC ACTCATGGGG CTTGGC  
 A/G  
 CATAGTGGGA GCTTGCCCAG TGCAGGGCCT GGCTCTTGCG TGCTCAGGAA ATGTTTGCTG  
 AATGGAATTT CAGTGGAATG GA

01T185 134bp  
 TTCAAATTGT AGATCTCCCC CTCCTATCTT CCACCCATA GCTAAGAAAG GAAACCCAGG  
 GATAGAACTA ATTGAACCTT ATTAGCCAG  
 A/G  
 GGCAATCGAA CCCAGTGCCA ATAGAGAGAT GGACTCCCAA TTAG

01t187 145bp  
 GCTGCAATGG CGTGCTGTGC TTGGGGGCAT GAAGTGTGCA GGGGTAGGTA TGCTGGCCCT  
 GAGACTTTCC CCCGTGAGAA TTTCATTGCC ACAGC  
 A/G  
 CCAGTGGGTG GATCGATAGC TTTAGGAAGG TGAGGTTTCT TTTGTGGAG

01T188 143bp  
 TAAAGCTGTA ACAGTTAACC TCTTCCACAT GCAGCATCTG CAGGCTGCTT CCCTTGACAGA  
 CAGTTTACAG TCTCTCTGTG  
 A/G  
 TAGTGCCAAA CTCTATGACC CAGGCCAAGA GTACAGTGAA TTTGTCAAGG CCACAAATTC  
 AA

01T189 140bp  
 CCAAGATCGT GCCATTGCAC TCCCGCCTGG GCGACAAAGT GAGACCCCAT CTCAAAATAA  
 GTAAATAAAT AAACA  
 G/A  
 AAAAGAATTT CTTAGACGAA ACCTTGTGCC TTTTGTGCTC AGTTGGATAG GAAGTGAGCA  
 TCTG

01T192 148bp  
 AAACATTTTT AGAGGCCAAG TGTTCATGTT CATTCTTTAT CCACTACAAT CATATACATC  
 AACTTTGAAT GGAGTTGTTT GTGATTGGC CTCATTA  
 A/G  
 GCTAAAATGC TTATGAAGAT AGATCTGCGG TTTGAGTAGC TTCAAATTTA

01T194 135bp  
 AAGACTTCTG AAGCACCAGT ATCTGAAGAG AAAGCAATGG AACACTGAGG AGAGATA  
 C/T  
 GAAGAAAGTG GGACCATAGA GGCAGAGAAA ACCATGAATG ACTATGCTTA TACAAGCCAA  
 ATGCAACATT TCAAGAA

01T195 132bp  
 GTAAAGGGAG TGGCCTGTTC AATATGGGAA AAGACTTGCC ACACATTAAA GCATTTTTTC  
 A/G  
 TCTTATAAAA TTGATGTATT CTTGGAAAGT GTGTAAATTC ATTTTACATG AAGGGAATAA  
 TTTTCATGTAA AG

01T196 142bp  
 TGCAAAATCT TGTATTGCTT GACTACCCAA GTATTAAGTAA AAATAGTCAT GCCCATCAGA  
 CACAGGCAGA GTTTATATAG TGAAACAAC T  
 A/G  
 AAACAGAGTT TATTAACAGC AAATATTCTT AACTCCATA GCACAGGAGT

01T198 116bp  
 TGGCATTATG TGCCTCTTGA TGTGATGCAC TAAAAAGGAT ACATCATAGA GTATTAAGGC  
 CAAATATGCA  
 C/T  
 AGATGAATTT AATCAGGAGA AAGCAATCAC ATAAATTGAG GAAAT

01T200 138bp  
 TTTACATGAT GATGACACAA AACTGTAAA GGACCTCTGG GTTACTTGTT TATAAGCTAG  
 TATTTCTTGA ATCAATTT  
 C/T  
 TCTGATCCCT AGATATTTGG TAGGTGAAGT CATACTATA TATCCCCACA CCCTAGAAC

01T202 139bp  
 CCTTTTCATT TGTCATTGTC TATCACTACA CTGTAAGTAC CACAACAGAT GGAACTTCT  
 CTGTTTGTGTT ATTAGT  
 A/G  
 TATCCTCACA ATATTTGTTA AATGAGTGAG AGACTCAGGA TACAAAGGTG GAATAAAAGC  
 AG

01T205 107bp  
 AGTGGCTTTT AAGATTCTCT TTTTGTCTTT GGATTTCAAC AGTTTAATT  
 C/T  
 TGATGTGTAT AGGTGTTAAT CTCTTTTGAG TTTATTACTA ATTGCAGTCT ATCTGGC

01T206 121bp  
 AGATGCTGAC CACAAGCCTA AACTATGAC CCATGCTTCT GGTAAACAG CTAAAAATTG  
 GGGTTCCC  
 A/G  
 TGGCCCCTTC CTCAGTTTTG ATTAATTTGC AAGAGTGGCT CAACAGAGCT CA

01T207 124bp  
 TGGCTTATTT TTTGCATAA CAAATTAGAA AGCAATTCAT AACTACAAA AGATCTGAGA  
 AGATCTGTTA TTTCTA  
 A/G

AGATTAATAT AGTCCGTGTG ATCAGAGGAA TGTCATTGCT CAGCAGT

01T208 120bp  
AATCGGAGAG CAGATTCTAG TAGTTTAGCA GAAAGCAAAA TAGAACAGTT AATAATCATT  
AACTTAGACT GC  
C/T  
GAAGGCACCT GAACTTAGAG TAAAGCATGA AGTGCTTGTC TTTGCCA

01T209 127bp  
AAGATAATAG CATGATGCTG CTATAAATAA ATGTATAGAT TGATATCTTA AGTGTTCTGG  
TGCTGAGTTA CTCA  
A/G  
AGAGAAACAG ATCTCTAAGT TTCTGGTGAT GAGTCACCAC GTGAGAGAAA TT

01T211 100bp  
GTTAAATGA GCTCAAGATG TGTAGACGTA TTATGTTTTT TTAGGCTA  
C/T  
TGTTTTTTTTG CAACATTTAG CAAATGAATA GGATAGTACA GGGCTTTTTT A

01T213 137bp  
ACGCCAGAGG CATGGAACAT TTTCTCCATC ACAGCTCTCA AAAGGAGTCA ACCCTACAGA  
CACGTCAATC TCAGACATCC AGC  
C/T  
TCTAGAACTG TGAGACAATA CATTTCTGCT GTTTAAGCCG TCAAGTCTGT GGC

01T217 134bp  
TTAATGAGAA AATGACCCAA TGATAATGTA TATGTAATTA AGATTTTCATT TGCTTCCCTA  
TACACC  
A/G  
TGAGAGTTAA TAAATATAAT CCTCTATGGG CAATTTCTTT AAATCACAAG AATATTGGTC  
CCTGAGG

01T220 126bp  
AATTTTCTTC ATAACACTGT TCTTCATTAA AAGGTAGCTT TATTTTATAT CTCAGTGATA  
AAAAGCCACC AAATCA  
A/G  
TTCTAGTTTT GTCAACTCTG TTGGTATGAG GAATCTCAAG ATTGAAAAT

01T221 120bp  
CCAAAGGAAG TCACATTGTT TTAAGTGTA AGTACAAGTT CAGAGGTAGA GGTTCCAAAT GC  
C/T  
TAAATTCTTC ATAGATTAGT CTTGCTGAAG TAAAGAATTT GAATAGGGGA CATAGGC

01T222 140bp  
CCTCAGGCC TCACACACTC ACCTTTCATT ATTCTTGCT TCTTGACCAT TCTTTATTCC  
TCATTAAGGC CACC  
C/T  
CACAAATGAA ACTCACCTT GAGTTAGGTA AAAACGCTCA TAAGCATAAT TTTCATCCCT GTGTT

01T223 103bp  
TAGGGCATCT TGACATCTGC TTTAGGCACA CTGAAATGTT CAA  
C/T  
GGCAAGAGTA TTTAGGACTG AGAACATCTG ACCACTCAGA GCAAATTATT TGAAGTTCT

01T224 141bp  
CAAAGCTAAA AGGGGCATCT GAGACAGATT TCCTTTTGTT TTCCTGGCG TGTCAAATGC CAC  
G/A

Table III

GTGACAGCAA AGGAATAATC TTCAGTTTGT GTATAATGAG GTCTGAAATT TCCGTGCGCA  
CATATTGATC ATGAATC

01T228 132bp  
CGCTAAAAAG GGAAAGCCTT CCTTCCTGCC CTAGGACATC CCTGCCAACT T  
C/T  
AGGGAGGTGG GAACCCAGCT GCGCTCTCTA CAGTATGGGT TACTTTTGTG TCTGGAAGGT  
GTCTGACATC CTGAGACCTG

01T230 142bp  
TGAATTGTAC CTTTAAAAAT GGTAAAGATA GTAAATTTTA CCATCTTCAC AGTTTCCCGA  
GATTGCAAGG CCAGCAGTTA AAGACAAAAA CAA  
AACTA  
T/C  
TTCCAACTGC CCTACAGTGT GCAGACCTTT CCCTTGTCTT GCCCTGAG

01T231 131bp  
TTTTCAGCAG TGATATTCCT TGCTATGTGT CATTCTATTT STATGGAACG GCCAAAAGAG G  
T/C  
GAAGCCATAG AGACAGAAAG TAGATTTGTG GTTGCCAGGG GCTGTGGGGA GGGGCCTGGG  
GAGAGATTG

01T232 142bp  
ACCATGAAAA TAGATGACAG AGTAGGCACA GGAAGACCAG TTAGGCCCCAT ACAGCAATCA  
AGGTAAGAGA TGATAGTGGC CTGGAACA  
A/G  
CACGTAGCCA TATAGGTGAC TATATTTATA TTTTGAGGGT GATCCAAAAG GAT

01T233 113bp  
GGAGGTTGGA GGGCAGGGGC AGATAGGCCC TACCTTTCCA TAGGGTGAGT GGCAAAGAAT TTG  
T/C  
AGCTATCTTT CACAACAGCT TGGTTAAGCA AAATTTTTTT TTACCATT

01T234 130bp  
GGCTATGCTA CAGTCTCTAG CTAAATGGAA GACACATTCA TCCTTCTCC  
C/T  
TCTGACTGCT TTGATCATCA TTTATTGCAT CTCATAACTA ATTTTCTAAA GTTTGGATTG  
GGACTTTTCA GGTCTTTTTT

01T236 128bp  
TTCTCTGGGG GAACCTGTCT CAGTGTTGAC TGCATTGTTG TAGTCTTC  
C/T  
CAAAGTTTGC CCTATTTTTTA AATTCATTAT TTTTGTGACA GTAATTTTGG TACTTGGAAG  
AGTTCAGATG CCCATCTTC

01T237 141bp  
AAAAGGCTAT GGAGGTCCAA CAAAGAACAT CCCAGCTCAG CAAAATGAGT GGCAGCTTCA  
GGTGCGAAGT GGCTCTGATC TAGGCGTTGA GGC  
C/T  
GAGTGGGATT TGGAAGTGTG GAAGTTGTGG GGAGGAGGCA TATTGCA

01T240 121bp  
GGCTGAAAGG ATGAGTGATT TTAAGGGGAA GATTTCTCTA TACTAGCTAG AACCTCTC  
G/A  
TCACGTCTGG CCCCTGTGAG CCTCTGAATG TGTGCTCCCT GGCTGAGCAG CTGATACACC  
CA

01T241 107bp

Table III

TGCTCTTATG TGCCTTTTTTC ACCTCAACAT GCAATGGGAT AATTAAA  
 A/G  
 AGGGTAGATT TTTTTTTATG AAATAGCATT TTAGATGAGG TAATAGAGGA ATACAGATG  
  
 01T242 141bp  
 ATTTGATCCA TTCATTGCTA AAGCAGTAAT TTTGAACCAT ACCATTGCTA AGTACTTAGT  
 CATCAATATA GGGTTGAATA GTTCATCTGA CA  
 T/C  
 TTTTGTTTTA ATTACTAAAA TGTTTTTTTG CCCAGTTCAA TTGGACCA  
  
 01T244 119bp  
 TGGAAGGGAC TGTCCTCCCT GCCTGCAGAA TCTGCTGTGG TATCTCTTG  
 A/G  
 ATGAGGCCAT GCAGCCCCCA CCTGGCTCCA CGTTCATTCT TGTCCTGATC CTCAAGCACT  
 CAGGGCCTC  
  
 01T246 99bp  
 CTTCCCTTCC CCATTTAGGA CTCTGACGCA GTACAGTTAA TCTGTGCA  
 C/T  
 AGGAAAGAAG AGCTGTTTGA AGAGGTTATT CGGTAAATGC AGAGAATGTC  
  
 01T247 143bp  
 AAAGAAATGA AAATGAAAA ACAGTAAATG AGGGAAAGG AAAATAATGA TGGCAAGGTA  
 AGGAGGAG  
 C/T  
 TAGAAGGTTA TGCAAAACTA GAGTTATGCA AAAC TAGGAG CTAGAAGGTT ATGCTAGAGG  
 TTATGCAAAA CTCA  
  
 01T248 120bp  
 GTTCGTGGAA GCTCACTGGT AGGTGAAGAT GCTTTCTGAG TGATAACATA TGAGCTATTG  
 CAAACATGGT  
 C/T  
 GGGGATTCCA CATGCCATTT AGCAATAACT TGGGGATAAT GTGGTACGT  
  
 01T249 149bp  
 TGGCTCTACT TTCAAAAGTT CTTAATTTTA ATATAGTCAA AACTATTTTT TCTTTGGTGG TAAAT  
 A/G  
 CTTTTCATGT CTTTAAAAA ATCTTCCCTT TCTCTAAGGT TTGAAGGATA CTAGCTTAAC  
 TTCTTCCACA GGTTTCAGAA TTT  
  
 01T250 136bp  
 ATACCATTCT ATCAAAGAAC GGCATTTGCT TTTTGTTACA CAAATTATTT CA  
 A/G  
 TGTTTAAGGA CAAAATGAAA CAAAACAGGA AAACCAAATT AACAAGAAAA AATTCCCTCT  
 ACAACCTTAC CCCTGCCCCG CCC  
  
 01T251 109bp  
 AAAGTGATTG TCAATATGGC AAAAAAGTTG GAGAGTGAAG TGTTTCAGTA TATGGATCTT G  
 G/A  
 AGAAATTCAA GAGCTAATAG AACTACGCA GGAGACAACT TGCTGGA  
  
 01T253 141bp  
 TCTCCCAGAA TTCCCAACAA CCCAAGGTTG CATTAAATTAC TTTTAATGGC AAAACCACTG  
 TTACTTTTGC ACCAA  
 C/T  
 CTAATATTAA CCTATTGTGG GAGGGACCCA TGGGGAGGTA ATTGAATCAT GGGGCCAGTC  
 TTTCC

Table III

01T255 139bp  
 TCCTAACTG AGTGTATGCA GTAGGTGGTC AACAATATTC ATTAGTA  
 A/G  
 ATTCTTTGTA TTCTTCCTGA GGGCAAACT GCTAAACTC CCTGGAGAAA AAGGCAATAC  
 CTGGCAAACA TAAGGCATCT CTCCAGGCTT A

01T256 139bp  
 CTTTGTGTTA ATGGCTGAAC AACTGTACAT ATCTGTAAAA CTCATTAAAG TATATATTTA  
 AAATGGGTGA ATTTTAATGT AGGTAAATTG TACCTCA  
 A/G  
 TAAAGATGAA TTTTTTTTTT AGCTGAGCGG GTGCAGAAAC AGTAAGGAAT T

01T257 114bp  
 CTACTGTAGC AGAAAGCCAA TAGAAAATGT CTAAATTTTA TCACTAGGAA GCAGCAATAT  
 A/G  
 AGCATATTAT TTAGGAATAT AATAAGACAT CTCGAAGAGT TGACAGTGGT TGT

01T258 115bp  
 CACTAAGAGG TAAGGCAGCT CAAAGGGCGT TGGCTAATGA AGTGGATTAT TGGGAGGG  
 A/G  
 TTTACTCTTA CGGGTTTTAG TGGGGGAATA CATTAGGTAA GATGTCTGCT GGGAAT

01T259 137bp  
 TCAACTTGGT GACTTATATA TGGAGAATTT CAAATATGTT CTAAGTGTTC GCCTATATAT  
 TTTTGGTCTG ACATGGGGA  
 A/G  
 AGAAGGTTTC TAGGGGAGAC TAATCTCTGA GCACTTACCA GGAGAGGACA CCTAAGG

01T262 139bp  
 AGAGGCACTT TCCACCTGGT TACCAACCAG AGTGGTAAGT GGCCATTGAA C  
 A/G  
 CTTTGGATAA CTTATTAATG GATGTATATG TGTTATTCTG CCTCTTCAAA ACCAGAGGAG  
 GGCTATGCTG TAATGGGCTT AGATCTA

01T266 149bp  
 GCCCTGAGAC TGTCTGCTAA TTTGGATTCT AGAACAACAC AATCCACCTT ACAAGTA  
 C/T  
 GTAAGGAGGA AAGTAAATAA CAAACGGGTA AAGTGCTTTG TAAACTGTCT ATACAAATAT  
 AAGAGACCGT TATTACAACA CAGCGGAAGA A

01T267 97bp  
 TAGAACACAC TGCCCGCAAT ACCCCCCCTT TCTTGCTGCG CCCTGC  
 A/G  
 GCTCCCGCGT GGAACCTCAT TCTTCCATTT GCCCCCGCC CCCAGTTGCT

01T268 108bp  
 CTTGTGGTGA TGGATATCCT AAATACCCTG ACTTGATCAC TGCACATTCT ATGCATGTAA CAAA  
 T/C  
 ACTCACAGGT ATCCCATAAA TATGTACAAA CTTTATCAAT AAAACATTTT TTAAAAAGAT  
 GTGCTTCTGA TCA

01T270 132bp  
 GGGGACTGTG CTTTGCACAC CGGCCGCGAC CTAGCCCTCT GCCCCCCT CAGTACTTCC  
 ATTTAGTCCC GTGGAA  
 C/T  
 AGGAGAGACC TGTTCCCAAT CTGGCCCGA AACTAGGGAT GGGGGGACTG TATTG

01T271 149bp  
ATTGAAGAAG AAAAAAGAAC AAAGTATTTT TTCCCATGT TTCCTGGTG TCTTTTCAA  
AGGTTTGTGT CTTAACAGGT GCCAAGAGCC TGCAATC  
C/T  
TTCCCAAACA GCCCTTTGTT CTGTGCTCAA GTCAACCCAC TGGGACTTTA C  
01T272 124bp  
CTGACTCCTT TCCCTCAACA TGCAAGCATG ATCAAGCCTT TCCCATTTTA AAGTAAT  
C/T  
TTCCAACCTTA CCTCTCCTTT CATCATCCTC TCTCTTTGGC CTTACCATCT TAGCGAAATT  
TATTGA

01T273 149bp  
CCCAGAAACC TTAAATATAG ACAGACTTTA TTAATTTATG TAGGAAGCCA AAAATAGGAA  
ATAAAAAGAT C  
C/T  
GGAGTTCAGA TATACTGATA TATTCAGCAA CTGAACTTA CAATTCCTTC AATTCAGTCA  
GAGCAGAGAC ATTTAAA

01T274 145bp  
CAAACCTTGA GGACTCATTC TGAGGCAGAG AATGAATAAA TC  
A/G  
TTACCTTTGT GAAGCATCAG AATCAGCAGC ACTTTCTGT CCCAGGAGAA GAGGGAAGGG  
GAGGATGGCA CGTTTCAGGG CTTAGGGGAG GATAGGGGAG AA

01T277 105bp  
CGCAAGCCCA GAAAGACGGC TGGGGGCAGG GGTGCTGCGT ACTGTTCAAT GAGAGCCATA A  
T/C  
GTGGCTGTAA CTGTCTTCCT CATATTGCAA GAACACTGCT GGC

01T278 124bp  
GGTGAATCAG GAAGATTTCT AAAGTCCTAG TTCTACAACT AAAGCATTAG ACGATTAAGG AAG  
C/T  
CCTTGATATT CTCTCAGAAC TTTCACTGAC CTTCTGCCTC CTACAGACTT CGAGGAAGAG

01t279 142bp  
GCTTGCTGT GCTGCTCCCT CTGCCCCACTA GAGGGAAGCC CAACCTCAGG CTGAGGCCTA  
GAAGGGGA  
C/T  
GGCTGCGCCA TGTGGGGCAG GGACAAGGAG GGGAGGAGAT GGCCTGCCAC TTCCAGACCC  
CAGTGCGAAA ACC

01T281 149bp  
ACCATCAGAT CTCATGAGAC TCATTACTAT TACAAGAAAA ACATGGAGGA AACTGCCTCT  
ATGATTCAAT TACCTCCACC TGGTCC  
C/T  
ACCCTTGACA CACAGGGATT ACGGGGATTA CAATTCAAGA TAGATTTTGA GTAGGGACAC  
AG

01T282 145bp  
AGGACTGCCA TTTTCTAATT CAGCAAGAAG TCAAGAAGTA TAGGATAGGT GTGAAGGATG G  
C/T  
GAGATCTGTA AATGTGTAAG CTTCATAACT TCTCTGTGAC TTGCTTAGCT TTATTCTGTT  
TTTTTTTTTG TTGGCAAAC GTA

01T283 137bp

Table III

AGCCGGTTGG TCTGGGCAGG AACGAAGTCT GTGTGGTCAA AGGGGACCCG CGCCGGCGAG  
 ACTGGGATGC TG  
 C/T  
 TTGGGCTGGG CGGTCAGAGT ATGGAGTGGG GCTGGGGTGA GGTGGCAAGC ACCCCAGGGT  
 GGGG

01T285 149bp  
 GTAGAACCAT GAACCAATTA AACCTTTTTT AAAATAAATT ACCCAGGTAT TTCTTTATAG  
 CAGTGCAAGA ACAGACTACT AATACACCTA GAGACCCA  
 C/T  
 GGGACACCAT CAAGCAGACC AATAGATACA TAATGACGTT CTAGAAGGAG

01T286 110bp  
 GGTTTTATGC ATTTCTCTCAA AACACCGACT GCTCTTCACG CACTTTCAAA CCATATT  
 T/C  
 CCTGTTCTCG CAATCCACTA TAGTGATCTG ATACATTAGA AAGCTGCCCT AG

01T287 122bp  
 GGTACCAGA GTTCCAATTC AATTAACACA ACTAACTGAC TATTGTAACT TGTAGACATT  
 ACCAATGGGA ATTAAC  
 A/G  
 CTTCTGAAAA AGGTTTATTT CTTCTCTTGA AGAAGAGATT GGGAGGAAAG GTATA

01T288 121bp  
 GTTGAGCATT TCAAGATCTT TCTCAGTAAT AAAATAAGTA AAGTATTTTA AAAATAGAAG TT  
 C/T  
 TCAATAATCA ACAATTTCGAT CTCGTTGATA TCTATAGAAT GCTCTAATTA ACGGAGAA

01T290 125bp  
 GTATGCTCAT TAAACATTA TTCGTTATAG AAAAAAAGTC TCATAAAATC TGGAAGCAAA  
 TGAATGTCA  
 A/G  
 TTAAGAGATT ATTTTTATCG AATGGAAATA TGAATCAGCT TAAATTGTGC ATTTC

01T291 146bp  
 CCCAATCTAA ATGTACATCA ACTGGTAAAT GAATAAAAAC ATGTAGTACA TCTATACAAT  
 GGAATATTAT TCAGCAATA  
 A/G  
 TAAGGAATGA AACACAGATA CAAGCTTGCA CTTTTATAAA CCTCGAACAT TATGTTGCAT  
 GAAGAA

01T292 121bp  
 ACTATTCTGT TCTAAGGTTG CACTCCAGGT TGAAATTGGC TGACAAGGT  
 T/C  
 TTAGCTTGGG TAGGATTTAT TCCCCATATA TTAAATTATT TTTTAAATTA GTTCAATGCC  
 CAGGTCATTT C

01T295 116bp  
 CTATGTCTGT CCCTTGCCCA TTTACCCGCT ATATTCTGTC TATATTTTC  
 A/G  
 CTGAATTTGG GTCCTGCTTC TTATGCTTTA TGACAATGTG TGGTACAGCC CTTTGAATCA  
 CTGTTT

01T296 143bp  
 ACCTGAAAGA AAGGAAATCA GTATATGGAA GGAATACCTG CACTCCCATG TTCATTGCAG  
 CACTATTCAC AATAGTCAAG ATACAGAATC A  
 A/G



CCGAAGTGCC CATCAGTGGG TGAATGCATA AAGAAATATG GTACATGTGC A

01T298 117bp  
 TTTCTGGTTG CAGCACTAAA AGTCAACTTG CCTTTTGTTG GCCTGC  
 A/G  
 TTGACCATTT TCTTCACCAA CTAAACACTT TCAACAGAAT AGATAAACTT GAATCCTAGA  
 TGAGATAGCA

01T299 142bp  
 ACATAATACA GCTGCCACAG CCCTATGTCA TTAAGCAGTT GAATTAATCA ACCACTTTGC  
 TACCCACCTC TGAACTTTTT GCTTTTGGAG ATAA  
 C/T  
 CCCCTTTTTG TTTAACCTAT TTTGTGTTGA ATCCTTACTT ACTCAA

01T300 124bp  
 TCAGTGACCC ACAATCCATT CCTAAAAGGG AGAGCCTCCT GTCTTTCTCT CAGTTCCCTC A  
 A/G  
 GCTCTTAGCA GGACTCAATA AGAGCCCCAG AAATTTCCCA GAAGTAGGTG ATTTAAAAAC  
 AC

01T301 124bp  
 TAGAGTAAAT GTGGTCTGCA CAGGTGTAGG AAAGAGTGTG GGAGAGGAGG AGGGGACAA  
 C/T  
 CTCATGCCTT TCTTTATTAA AAACACATAA AATAAACCTT ATAAATGAA AAAGTTCCAT  
 GGAT

01T302 103bp  
 GGAGCATTTT TTGGTATCTT TATTTTTTAG ACCACATCCT TCATGGTTGC AT  
 G/A  
 TTGTTCTATT TTCTTAGGAA TGCCTGAAG CTTGGCTTTG CTTTTATGTT

01T303 90bp  
 AGGATGCAAC AGGAGCGGGG TTGCCTGATA AGACAGCGAT AGAAAACC  
 A/G

AGAGATAAAG GAAGTCTGGC CAGCAGCAGC TAGTCTAGAG G  
 01T305 106bp  
 GAAGGGTGTG TGCAAGTGTA GAACAAATTC CTTCCGTGAT TAGTCAAGCT ACCTGACTT  
 T/C  
 AAACAAGTTT TATTTTTGTC TCTATTACTG TTAAACTGCA TGGCCT

01T306 115bp  
 AGGCTGAAAT GGTGTCATGT GATTCCAGAG GCCAAAAGGC TGGTGTGGAG TCA  
 C/T  
 GGCAACTTTC CTACCACTAC ATTCCCCCTT CCTATGAGTT TCATCGTACC AATGATGGCT  
 G

01T307 115bp  
 ACAACTGTGA ATTGTGGCCA AGTCTCCCAA ACTGGTTTTG TTCAGTTCTG AACTTGCAA  
 C/T  
 ACACCAGAAA TTTTAGGGTT TGGAAATTAG GAGATCAAGA GTTTGAATGA AGAA

01T308 115bp  
 CAGACCAAAA TACATTTATG ACACCTGTGA AAGTAGAGGA AGAAGAAAGG TTTGTGTAGG  
 AAGAGTCTCA GA  
 C/T  
 CAAAATCAC TTCTATGAAA GTTTCAGCCA GGGCCAATGG TG

Table III

01T309 131bp  
 AAGAAGCCTC CAGGAAAACA CATCGCTTGC TCCAGGAGTG TGTTCACAGA GTGTCGACAC  
 AGCTCCAGC  
 A/G  
 TTTCTCACAG CCTCTGCTGC CAGGAAAGGA TAAAACACCA CCCATATTCA GGAACAAAGA  
 C

01T310 135bp  
 GCCCACCCTA ATGACCTCAT CTTAACTTGA TAATCTGAAA GCACCCTATT TCCAAATAAG  
 GTGACATTCA  
 G/A  
 AGGGTGTTAG GACTTCAATA TCTTTTGAGG GGACACAGTT CAACCCATAA CACCTACCAA  
 CGGT

01T312 145bp  
 GACACTCTGT TGAGATGGGG GTTAGACATC TAGGTACTGT TCCTGTTTCT CTAAT  
 A/G  
 ACTAGCTACA CAATTGTGAG CACATTGCTT CTTTATCTGT TTCTCTAAGT CCTTCTTCAT  
 CAAAATAATT TGAATTTCCA TTTTGCTGG

01T313 134bp  
 CAAAAGAAGG AACAGGGAAT ATACCTAGAC TTTAACCTTG TT  
 A/G  
 ATACTATAGT ACCTGTCCTG AGTAGTACAT TGTAGAGGCC AGCCTGACTA ACTGGAAGTC  
 AAAGGAGAAA TACCAAGAAG AGGAATGGCC T

01T314 110bp  
 AGGGGAGAGT TTCTTTTTAA GTTATTATTT CATATTTTCAT GGATTTTCATG TCTTCCTCTG  
 TCATTT  
 C/T  
 CTCCAAGCTC AGTTTGGGGA ACCAGCAGTC TGTGTTAGTT CAC

01T316 143bp  
 ATCAGGCTCT ATTAATGGT GGTAGGATAT GAGGCTACAG ATAACAGCAA AAAAATTAAT  
 CAAAGTTTCA ATTA  
 A/G  
 CACAGTACAC ACAGATCAAC CCACCAGCTA TTATGTATTA GTTTTAAGCA CTTGTCATTA  
 TGCCTCAT

01T317 146bp  
 TGGAATACAC AAATTTTGGA AATAAAAGGT TCAAGTTCCA ACATGCCAAA ATT  
 C/T  
 TACTGAAAGT AACAACTATA TTAAAGCTTG TAGTGACCAG GTACAGTAGC TCATGCCTGT  
 AATCCCAGCA CTTTGGGAGG CTGAGGCGGA TA

01T319 136bp  
 GTTTACAAAT GAACTCCTTT TCTGTCTTTG CATTTTATAGAG AACTAAGTG ACTAAGGAGG  
 AATGTCAAGG ATCATAGTGA CAA  
 C/T  
 ATGTTCTTCA AACGAAGCTA GGAGACTGAG AGGGAAGTGA TGGAGGGCTG AC

01T320 145bp  
 TTTGGCTCCT CTATGGGCAC AGCTGGCTCA GAGGGCTCTG AGCAGCATCT TTCTATTCTG  
 GGAAACTACA GCCAC  
 G/A  
 CGCCCGTGTG AGCAAGTTTG CACCATCACG CTCTGAGACC AGAGTCCTGC CCTTTCTCCT  
 CCTCTGTGC

Table III

01T321 133bp  
 GCACCTTGTTA GAAACACGAA ACTCGTGGGC CTGACTTCAG ACCTACTGAA TCAGAAATAC  
 TGGATGGGGC TCAGCAATTT G  
 T/C  
 TTTTAACAAG CTCTTAGCTG ATTCAGATGA ATGCAAATGA CTCTTAACCA C

01T322 141bp  
 TCTTTTGATC AAAGCAATTT TTAGTTAGAA GGAAACAGCT GACTTACAAA GAAATTGCAC TGAG  
 A/G  
 CTATTTCTAA ATAAAAGTGT TTTTGCTGTG GCATTGCAGG GAATTGAGGC ACCTTCCATA  
 CTGGTGGTTA CTTACA

01T323 118bp  
 AGTTTTCTAC AGAAATCACT CAATGAGCAT TGATGGCCTG AAATGAATTT  
 C/T  
 GGCTTAAATG GTACAAATGT TCAGAAGCAG GAAAGCTCAG GGCAGGTTTG AGGAAATTAA  
 GCAGTCC

01T324 129bp  
 CAGTTGAAGC CACTACAACA TCTAATACAT CAGCCTTGGA AGCCATCTTG CAGATCATCT CATC  
 A/G  
 TGGGAAAACA CACAATATCG ATGAAGCAAG CGATAATGCT CCACACACTG TCGGCCTAAT  
 GGCA

01T326 133bp  
 GCATAACCCC AAAGGGTATT CTTAGGATTT GTAGGTAAGG GTTTGAGAAG  
 A/G  
 AATATGTCGG CTAAATATG GAGAGAACT TTTAAATGCA GTCAATAGAT ATGATGGACT  
 GCATTAAAT ATGTTGAATT CC

01T327 132bp  
 TGTGCTTTGG TTTCTTCTCA GACTGAAAGC TGGACTAGGG AGACAAGTGC TAGAAAATGA A  
 A/G  
 CATAAAGCAT GAAGGGTATT TTTTTTCTCC GTTAAAGAA CATTACACG GTCCCTAGTG  
 TCTACAAAAG

01T328 146bp  
 GTGTGTCTCT GACCTGGGCT CTGATAATAG GACCCAAAAT CCCATCTTCT TTC  
 A/G  
 TATTGGGATT CACTGTATGT TTGGTGAAGG ACTCATCTTC GTACTGTGTG TACATAACTT  
 TCTTATAATG TTTTCCAATT TGGTTTGAGA AA

01T330 111bp  
 AGTGACAACT TAGACATTTG GTGAAAACCTC ATTTTCATTT TATATG  
 A/G  
 TAGCAGCAGG TTGTGCAGGA CATGAAGGCT ATACAGTTTT GTGAGGCCTC CTTAAGTAAA  
 AAGT

01T331 136bp  
 ACCACTCACT CTTTGGGTCC GTGCCATCTT TAAGAGCTGT AACACTCACC GC  
 A/G  
 AAGGTCCATG GTTCATTCT TAAAGTCAGT GAGACCACTA ACCCACTGGC AGGAACGAAC  
 TCCAGACACA AGATGATGGA AGC

01T335 139bp

Table III

CAGCTTCCAG AGACAGGCTT TTGATCACCA CAGGGTCCTT CCCTTTGTCC CAGTTATCCC  
 AGGGAAAGCT ACTAATCTGG TTCAGGTGG  
 A/G  
 CGTGGGCAGG GGCTGCTAGG CCTGCAAGAA GCAAGCCCAG GACAATCAG

01T336 134bp  
 AAGTTGAATT TAACAAGCCT TCTATTAGAC TTGAATGCCT GCATTATGAT AATTATAAGC  
 ACACCTTTCA CCAGT  
 G/A  
 TAATATTTTT CCTCTTAGGA GCTGTATGGC AAAAGAAGT TTTGTGAAAT TTTATTGC

01T340 127bp  
 CCATTCTAAC TGGTGTGAGG TGGTATCTCA TTGTGGTTTT GATTTGCATT TCTCTGATGG  
 CCAGTGATGA TGAGCATTT  
 T/C  
 TTCATGTGTT TTTTGGCTGC ATAAATGTCT TCTTTTGAGA AGTGTCT

01T341 108bp  
 GAAGCTGAGG GAGCCCTGGG GCGGTGGGAA ACAGCGCTGA CAGTTAGAC  
 C/T  
 GTAAGAGCCC AGGGTAGGAA CTGGGCCCTT CGCTCAGTAC CTTGGGCCAG GTCTGGCA

01T342 149bp  
 TTGGAGGTAT CATCTTGACT TCTCTTCTGG TCATGGCTTG TTACAGATTT GGCACCTTTC  
 ACTTGAC  
 C/T  
 TGAAAGGAAA CAGATTTTAA AATTACATTT AATTAGTTTG CAATATGAAA CAAAATGAAG  
 CCAGTTTTTA AGACAATAAG A

01T343 109bp  
 AGTTTCAGAG TTCAGCTTCA AAGCTAAATG TAATCCCCCG TCTC  
 C/T  
 CCTTCCCCTA CAATAGTAAA ATGAAGAAAG CTATTTATTT CCAA

01T344 113bp  
 TTTTGAAACA TGCAGCGCAA AAACCTCAAAT TTCATAGATT GACTTTGTTC TTAACAGAAA  
 ATCTCT  
 A/G  
 TGAAAGGAAA TTTGTGAAGT AGCAAGAGAA AAAGAAAAGC ATGGTG

01T346 132bp  
 ATTAACATGG AAGGGGAAAT ATGATAGATA TATAAGGACC CTCCTCCCTC A  
 T/C  
 TTATATTCTA TTAAATCCTA TCCTCAACTC TTGCCCTGCT CTCCGCTCCA CCCCCTGCCA  
 ACTACTCAGT CCCACCCAAC

01T349 126bp  
 GTGATCCTTT CAAAAATGGA TTCAGAAATC ATGTCACTGC TCTGCCCAA GTTCCC  
 A/G  
 AATGACTTCC CAGTCACTCA GAGCACAAGC TGACGCTCGA CACATCTGGG CCCCCTAAGA  
 TTTTCATTT

01T351  
 ATTCCAAAGTTTTAAATTTTCCCATTCGTGTCATAGTTTGGGTACCCTACTCCTCAGACC  
 CGGGGCGAGCCTTCGGCTGTGACTCAGCACATAAAAAACCAGAACGCCGGAAGTATTTTC  
 CTACACCCGCCGGATG

A/G

ACGCTGCTCCCGAGCGCCGCAAATACTAATTGGCTCTTCTCTACCCCTACAGTCGGCCCCGA  
CAGTGGTGGGGTTTCATCCTCAAGCCCTAAGAAAGTGCTAAAAAGACCAGTCTGGATGTG

01T353 110bp

AAATTGTCTT GGAGAAGCCC TCAGAAGAAT AGGGATAGTC TGTTTGAGCG TGTTGTCAAC C  
C/T  
TCAGTCTCTCT CTTGTGATCC TAGTTAACCT TCCCTGGTTG ATAAGATTC

01T354 102bp

CTCTCCTCAG GCCTGACTGG CTATGTATTT TCATAAGTGA AGAATTT  
C/T  
CTGGTGAATT CATGCGATGC GTTCATCAGA GAATAAGAAA CGCAAACCAT ACTG

01T355 142bp

AGGTCTCATC TTCTTCATGG ATACAGTAAT GCTAATAGAA CCCTCCTATT CCATAGTGT  
C/T  
GGCTGCTGTG AAGGAGAAAG GCAATACATG GGCTACATAT TACATAATAC TATGTAAGTA  
TTAGCCTTAT CATTATGGGG GC

01T359 113bp

TGTAGGTCAC TCTATCTCTT CAAATACCCT TTAGTGGTAT TTAAGGTTTT TGCAG  
A/G  
GTCTGGGGAC TTAGGTGTTT CAACTATCAC CATGGATTTC CAGATTTTGT AAAAGGT

01T361 123bp

GAACAGATGG TAGCCTGTGG TGAAGGTCT CTTTCAGATC TTTAGTCTCT TTTCC  
C/T  
GTGAATTAAT CTTACCTAGA TCTGGCCAAG AGGAGCCTCA GAGTAAGCCT ATTTGCATCT  
GTTATTT

01T362 117bp

TTTCATTAC TTTCTCTGTG CTTAACAAGG CAAAGGGATT ACTGTGCT  
G/A  
GGGTTACTGC TATACCAAAC TGTCATCTCA GTTCTTCTTG GATACAGTCA GTTTAATTAT  
GCCTGGTT

01T363 141bp

AAAACATTCT GCCAGTTATG GTCAGGGAAC TGCATATTTT TAGCTTATCT TCTTCATTGT AAA  
C/T  
TCTCTAACAC CTAGAACTCT ACCTACCCAT AGTGGACACT CAAAAATAAT TTGCTGAATG  
AATAGTAAAT GTGGACA

01T364 135bp

GCGCAGGGAA TACACAAGGC TTAATCCACT AACAGAATAG GTTGAAAATA C  
T/C  
GAGATTCACC CTCCACCCCA ACAATGCAAG GAGACTCAA GAAATTAATG ATCACAGGCT  
GGGTTTGTGA TGAAAGGAAA ACAA

01T366 129bp

GCTGCAGGGC TCTGCTGCTG GTCACCCACG CTGCAAAACC CAAACCT  
C/T  
CCTCTACTGG GCCCTCAGTT TGCGCACATA AGGAAACCCA TTGCCTTCCT TTAATCAGAC  
TAGGGCTCTA ACCTAGTGAA C

01T367 147bp

GAAC TTGGAA ATTGATTTGC ATCTAGTAGC AGACAGGGGC TCCCAACCTG AGCACAAC  
A/G

Table III

TACCAGGGGA ACTGTGGCAA GAGGCTGTTC TCACAGTCTC TTCCTTGGC TGAGGGATAG  
GCCTAAAAAG ATGGAGTAAA CGACTCCA

01T371 122bp  
TCATATATGC ACATTGCATC CTAACCACAC CAGACTTTCA AGAGCCTTTG CCTTTGTTTT  
TCAGAT  
C/T  
TTAAACTAAA TCTTATCTAA CACCACCCCA TCCAGGACCA TTTTGTTTTG TTTTT

01T372 114bp  
AAAATGTCTG TAAATTACAG CATCTATAGA CAGCTATGTT TGCAACATCC CTTTAACCAC  
G/A  
CTATGATATT TGCTAACCAT GCTAGTGCTA TTTGTTCTTA TTACAGACCC AGA

01T373 125bp  
TGTAACATCT AATTTGTGGC ATTGAGTAAA GTTTAAGACT TGTCAGACCT GCCTTGG  
A/G  
AGGGATAGCT TCCCCACCCC TTCCCCAGCC ACAAATGGAA TACTGCATTC CACAGTGAGA  
ATGTGGC

01T375 104bp  
CTCCTCCATC CACTTAAGGT AATCACAGCA CTGTAAGGGG CTATATCAAA ATTC  
G/A  
GCATCAGCAA CATAAATTTG GTTGACAACT GAGCTGAATA GAGGACCTA

01T376 128bp  
GCCATAGACC TCTGCAAGCA AAGCGACCCC AAGCATTTCT TTCTGCCTGA ATAATTA  
C/T  
GGTTCAGTTC ATCTGTGATG AGAGATATCA GCCCTGCCAC AGCTAATTAC TATAGGAATT  
GGCCTTCAGT

01T377 131bp  
CTGAAAAAGG TCTCTCTGGC AACAAAGCAA CAAGGTGGAC ACTGGAATGT GAAGGTGCTA  
GAAGAC  
C/T  
ACAGAAAGTG TATTTAGAAG AATGGCAGCA GCCTGGAAAA GCAAGGATGG GGAATGAACC CAAG

01T380 127bp  
CCATGAGGCA GATAAGGGAG TATTTACAGA GGTAGGTTAC ACTGGACCTA CCT  
C/T  
ACGGGCTTGT TATAAGGTTT GGTAACATTG AGAAGCTACT AGGCATCACT GCACTATATG  
CATTCCATAT GCC

01T381 126bp  
TGAGAATTCT GGCAAGATTT TATTTGATGA AAGTATTCCA TGGTAGTAGA ATACTATG  
C/T  
GGCCATAAAA AAGAATGAGA TCGTGTCTTT TGCAGGGGCA CAGATGAAGC TGGAAGCCAT  
CATCCTC

01T382 135bp  
ATCATCATTC AGCATGGATA TTATCATCGA AATTTAAGAA AAGGTATG  
C/T  
TATGTATTTT AATGGCCTCT AGTGATTCTC CCAGTCCTAA GATTCTATCA TAATTTTAAG  
TAAAGAATAT GCCGCATGCA TAATTT

01T383 113bp  
CTAACACTTT CCTCTTCATG GGGATAACCA TATCTGAAGA ATGTTTAC

Table III

A/G  
 TAACTGCATA ATCGATGCTT CCTGGACCTT CAGCCCAACT TTAGATCTCT GGGGGATGGC  
 TTTA

01T387 149bp  
 TGTTGAGGAG ATGGGCACTT AATTGAATGC TTAAAAGGAT ATTTTTCCTA AGCTTTTCTT  
 GAAGCTTAGT AT  
 C/T  
 ACTTCTTAAT CACTGTACTT GACAAGTCAA CCTTTTAATC GGAGCCTGAT AAATCCATAA  
 CATAAAAAAT TGCATT

01T388 140bp  
 CTCCAGTAG GACAAGGGAA AGAATAAAAT ATCTTATCTC CCTGTAGTGA GAC  
 A/G  
 GCTTTATTAA GATTTGACAG TAGTTATTTA ACAGCAATAA TTGAGTTTTA TGCAAGATTA  
 TACACGTTCT CCTAATCTGG CATCAA

01T389 149bp  
 CCAAACCTGC AGAGAACCTA TTGGTCATTA GCGATGAGAA TGAAGTCAAG TGTTTATTAC  
 TGATTACAT ATAATAAAGG TGACTAACAG GGTG  
 G/A  
 CTCATAACCC AACAAATTCTG TCTCCTCAAC CTGGAAGTCT ACGCCTTATC AGAG

01T390 124bp  
 CCAAGGGTAT TAGTCAGCTC AGGCTGCCAT AGAAAGATAC CATAGGTTGG GTGG  
 C/T  
 TTAACAACAG ACTTTTATTT TCTCAATATT CTGGAGGCCA AAAGTCAAAG ATCGATGTGC  
 TCACAGAGT

01T391 148bp  
 ACAATCACAA GGTCCACAA TAAGCTGTCT GCAAGCTGAG GAGCAAGGAG AACCAGTCTG  
 AGGAGCAAGG AGAACTCAGG AA  
 T/C  
 TTGGAGTCTG TTGTTTGAGG GCAGGAAGTA CCCGGCATGG GAGAAAGATG TACACCAAGA  
 GGCTA

01T393 141bp  
 CCCTATGATG TTCCCTCTCT CCCCTCAATG ACTGTAGCTC TCTAGTTCTC TTTCTACTAC  
 ACATTCA  
 C/T  
 CACTTAATAT TTTGTACTGC TTTCTTAACT GACAATAAAT GCTGGCCAAT GCTTTCCCTG  
 TTTGTGCACA ATA

01T394 137bp  
 TTCTTTAAAT CAAGCACAGG GCAACATTGA ATACATTTTC CTACTTTATA TAGCATTTCT  
 GCAAGTGCTG GGGTTACATT TTAGTCTTCA  
 C/T  
 AGAATGCGTG ATTCAAAAGT TTATTTTTTT GATTTAAAGA CACGAA

01T395 117bp  
 GATTTTGGGA TATGGTGAAA CATAGAGGTC TAGTTTCATT CTTCTGCATA TGAAAATCCA  
 GTTTTCCTAG AAC  
 T/C  
 GTTAATTGAA GAGACTGTCT TTTCCACAAC ATCCCTTTGT CAA

01T396 133bp  
 GGCTGAAATT TCACTTCCTC AAAAGAACAT TTTCTTGACC TCTAACA

Table III

C/T  
TCTAAATCCC ACCCACTCCC TGCTTCATGT ATCTCTTTTC TGTAGCACTT GCCATAGTGT  
AGGTTTACCA TGAATTAGTG TGATT

01T397 145bp  
CCCTGATATC AGCTAGGGGT CATATGGATA CTGGCTTGCC C  
A/G  
TGTGCTAGAA CTGGGCACTG GGATGAAGGA ATTACTTCAA CATGTGTTTG GATAGTTCTA  
CCCACCTTTT GCAAGGAGGT TGGTTTGTGC GTCTGCAACG ACC

01T398 149bp  
GTCCCCACAC TGGGCTTCTG GACAGGTGGC TGCCAAGATG GGGGGACCCT GCCCC  
C/T  
GAGGCCTCAC CTTGACGTTG TGCATGCTCA TGAGGTTCCC ACAGTGGTCC AGATACTGCT  
TCAGGTCAC GTCTTGGAAAC ACAGAGCGTG GCT

01T399 144bp  
AAGGCTGGGA GGTGCCCCCA TTCTCTGGGT TGGAGCGTGA TGGC  
A/G  
TCATCTATGG TCGGGGCACA CTGGACGACA AGAACTCTGT GATGGTCTGA GATGCAATGT  
TCCCTCTGCC TTGGGGCCCT AAAGATCAAT CAGGATGGG

01T400 147bp  
AAGCTCTGAC TTGTCCTTGG CTGCAAAGAC CTGAGGTCTT CTCTTTCTAA GGCTCCTA  
A/G  
AAAGTGTCTT CTTGCAGCAT CTTGGCCAAT TCTCACTGGA GTTCTATTTG GAACAAGTAC  
TAAAATGCAA GCCAGAGTCA ACAGAAGA

01T403 131bp  
TAAATAATCC TGCAATAATT CCTGAAAAGT TGTAATCAC TGACA  
G/A  
TGAGCTTGGG GTGTTATCTC TCTCAGGGAC ATTTGTATTT TAATAGGAGT CTCATAATGC  
TACAAAACT TTAATCAAAG CAATT

01T404 137bp  
CAGCCACAAA TCTGGTCAAT GAAACACACC CAAGAACCTG TAAGATTATA  
T/C  
GCCAGGTTCC ATGGGAAGTG CACTTGAC T TCTCTCCCAA GCAGTGAGTA GACTGAAAGT  
TTCCAAAGGT GGGGTTTTGT GTTACC

01T406 125bp  
AACCACCTGA TGACGTGTGT ATTAAACAAA CAAACATTTT GAAGTGCATT CTTTATAAGG  
TAAGGCTTGG GAGGAAAGC  
C/T  
GCCCACAAAT AACCTAGGAA TTAAAAAGGT AAGCAGAAAC AACTT

01T408 124bp  
GCCTCAGTTT TCCCCACTGT ACCATGAGAA TAGTAGCTGT ACCTTTCTCC TAGGGTTGTT  
GTGAAAGTTA AAT  
A/G  
AATTAAGGTG TACATGCTGG TGCCTGACGC ATAAGTGTGC TACATGTGTG

01T410 109bp  
CTGGGCACTC CCAATTTCTA GTCATTCAAT ATCTATTTTT CTCCTTCTTT TCTTCA  
A/G  
ACCTTGTGTC TTTCATTTAG TTTCTCAATT CATACAAAAC CGCATCCAGG AC



01T411 148bp  
 CAAAACCTGC AGGGCCAAAA CAAATACAAC GCATCAGAGG CCCCACCTCC TAACCAAGGA  
 AAGGGTAAAG GCAAGAATAA CACCAAGAGG CCACCAGCC  
 T/C  
 CCCATCAGAC GGGCAGGACC ATGGCGGCTC CTAGCACATA AGCCTCGG

01T412 104bp  
 TAAAGCATT CCAAACAAAC ACAATTTAGG ACAATTTGTG ACA  
 C/T  
 ACATTTGCTT TAGCTAAGAG ATGAGGATGA TTCAAATTG AACCATAACA CGAACATATC

01T414 121bp  
 GGGAGATGAA GATGACCCTA TGTACATCTT CCAGTCCAAT TATAAGGCA  
 C/T  
 ATATGGCCAG CCATGTGACC CACATGCCCA TAATCAACCC CAAGGAGAAG TACAAGCACC  
 TAGCCATAAA G

01T415 133bp  
 TCTGGGGATC TCTTAGGTGG CTGGTGATTC CTCAGAGCAT TTTCCAC  
 A/G  
 CTTACCAGCT TTTCTATTAA AGAGGTTTCTG ACTGTGCTTT TCTGTGCAGA AATGTTTATG  
 TCTTTTTTTT TTGAGACAGG GTCT

01t417 134bp  
 GCACACATTT AATTTGTTTG CACCAAAAAA GAACAGTAGA AAACAGTCAT TAATTTAAGG TA  
 A/G  
 GAATATATCA TCCCTGAATA CAAAAGTAGG TATTTACGGG TCAAATGCAG AATATTCAGT  
 GAACAGTTTC C

01T418 132bp  
 CCTGTAGGGT CACCTGGAGC TGCAACAGGG AATTTTCTCT CCGTATACCT AACTG  
 A/G  
 CCAGAGCTTA AAACAATTCC AGATCTCCTG ATCTATTGG CTGGATAACA TAAGAATGCT  
 ATTTTGGTGA AGGTGA

01T420 135bp  
 CTCCAGAACG GGCAACATA TAGAGTCAAA GCAGATTGGT GATTTGCTAA  
 G/A  
 GGCTGCAGGA AAAGAAGATA GGGATATTGG GGATGATGGC TAAGTGGCAT GGGGTTTCTT  
 TTTGAGGTAA TGAAAATGTT CTCA

01T421 123bp  
 AATTCTTCAA ATCACCCTGT CGAATTGGGT GAATTAAATA GGGTTCTGTC CCTAAACTGT  
 GGCTTCAGTC AG  
 A/G  
 TCTTATCTTC AGTCTTTTAG GTTCCCAAGG TTTGTGCAAG GGCTATCATG

01T424 124bp  
 GTCAAAAGAG GTCATTTTGG AACTTTAAGG TTTAATGAGT GCCCTATTAA ATTTT  
 G/A  
 GATTGTCATA GGACCTGTGG CCCCTTTGTT TTGGCCAATT TCCATTTGGA ATGGGTATAT  
 TTACCCAA

01T425 145bp  
 GCCTTGGTAA GAAAGGGATG GGAGACAAGG CTAGAATGGT AAACAGGGTT CAGACTACAG CTAC  
 C/T  
 CAGTGGTGGG TCTAGAAAAA TAATGACCCA CATAGAAAAG TTAAGTAAAC ATATGATCGA

Table III

GGAGTTTTC A TAAAATAACG

01T426 149bp  
 ATGCGTCTTC CCAAGGATAC GATGCACCCA CCTTCCTTCT GTCC  
 A/G  
 GTACCTCACC ACACCCCGTC TTA CTCTGGG GCTTTTCTTT TCCTTGCAACT GAGA ACTAC  
 AGTTCTCTCA ATTTTATTTC AACTTGGGGG TTGTCACCAG TGTT

01T427 131bp  
 ACTTCCTGCT CATCATCAAA CAGCCCGCCA AATCCAAGTT AAAGGATCTC CATCCCAACA  
 TCCCTCTAGC TAGATCCTGA ATCCCC  
 C/T  
 GTGGCTACCC CTGTCCCATG TAGAGGGAAG TGTA ACTAAG GGAA

01T428 109bp  
 GGGTATATTC AGAGAGTCAT GGTAAATGTT TCTTGCCACT AAGAGAC  
 C/T  
 GAAGACTGTC GTCTGATCTA TGCAAGAGAG AGCTTAATTA GGCATAGACT GGAGTCTGTT  
 T

01t429 93bp  
 ACCCACATTC ATTACCCAAC TCTTCATCTG AACCCTGTGG TG TAGACA  
 T/C  
 GGGCTAGAAA GGCCAGAATC CAGTCTTTTG GAATGCATGT GGCA

01T430 149bp  
 TCAGTAGCAA ATATGAAGCT GTTACATACA GATACTGAAT AAAGGTTAAG TAAAATCCTT  
 CACTCATTCA ACAAATATTT ATT  
 A/G  
 CTCTAAGCTT GGTGCTAGTA TATCAGACCT AAAATTTAGA GTGCCACCTT AACATCTTTG  
 AGCCG

01T431 121bp  
 TGTCTATTTT TGCTTACGTT GCCTATGATT TTGGTGTCAT ACCTAGGAAA CCATTGCCAA  
 AAGTAATATT TTTT  
 A/G  
 TATAGTTTCA CAACGGAATC CCACATGAGG AACAGAACAA TCAGTA

01T432 115bp  
 GAGGGGCATG GCCAGGAGAC AATGACAGCC CAGTGTCAGA CGTGCTTTAG TGTACACACT  
 TAGAAG  
 G/A  
 TACCAGAGAT GTGTAGAAGT AGAACTACCT AAATCTGCCT GGAGAAGG

01T433 142bp  
 TCTGTGCTAG ACATGGTGAT GGGCACTGCC AATTAAATCT GTATTATAGT TTAAAGCCTA  
 A/G  
 GAAGAAATTC TCAAATCCAT TTCACCTATC TTAAATCTTA GCAAACCAAC CATACTGTGT  
 CCGGGATTGG TTCCTTCCGG T

01T435 126bp  
 CCCCTTTGCT TGAATTCTTA GGCTTTTGTT CTATACTGAG AATCAGCCAG TGCTCCTTAG  
 GGGATATACC TTGAA  
 A/G  
 AATATCAACT CATCTGTCTG AGATTCCTTT GACTTCAGGA TCTTAACTCC  
 01T436 148bp

Table III

AATGACAATT TCATAGCTTG GGCTTTGATG GGTAACCTGC AGCCCCACTG GCC  
G/A

CTCCAGCAGA TGGTGACCTT GTGGGTGGTA GAGAGGCTTG AAGGATCTAG TGCATCTCAG  
CTGAAAGTGG CTTGTCTCAA ACAGATGTGA GAAG

01t437 142bp  
TCTATCTCAA GGACTGAGTT CTTTCCTGGA AGCATAGCTA GGACTTTTGT TATAGAAGCA  
AGTCAAGGAA GAGAAAAATT TTAAAGAG  
C/T  
AGATAAAGGA AATGGCCCTA GAAAAGTGAC TCCCAGGCC ACATCAAATA CTA

01T438 129bp  
CCCTCGGTTG TCAGTTGCTG GTTTTGCACA CTGCGTCAGC TTCTCCC  
A/G  
TGTGCCTCTC TGGCTGGTGA GCCTTCATTC CCCCTGACT GGCTGCCCTG TCCCTCTCTT  
ATTAAAGGAT GCCTTGGGCA C

01T440 145bp  
TCTTTTTTGG TCTCCTTTCA TCACTGTGTG ATTTACTTTA ATAGTACCCT GTCAAACCTAG  
ATGACTCAGT GGCCTCATCA  
C/T  
AGCTTACAGA GCATTTTCATC TGTGGTCATT CATCCTGCCT ATGAAGAAAT TGACATGTAG TCAC

01T441 149bp  
GGTGGGGTCT TCCTATCTTA GACCCCTGTA TTATATAAAG GTACACAGTG CACCTCTTCA  
TAACATTCAG TAGT  
A/G  
TGACTAATGA CTCACTGAGT CCCTGTTTTT CCCATAGAGT TCCAGGCTCC ATGGAGTTCC  
AGGCTTCATG AGGG

01T443 140bp  
ACTCAGGGTC CAGCTCTTAT GCTCCTGGAA CAGATTGTTC CAAGGTTGAA TTCAGACCGC  
C/T  
GCCATTTCTT TGCTCCAGGC TAATCTTAAA TGTTCCACCT GGGACACTGC TTGCTCCAGC  
ACCACTCTTT GCTTATACT

01T444 133bp  
GTCAAGTTAT GCGGAAAATC CTATTAGAAG TATTTCTTGG TATT  
A/G  
GACTAGATTT GTAAGTTGAT TGGGTGCAGT TGAAATCTTT AAAAACCCT ATTAAATTTG  
TGGATTTAAG CCCAAAAGAC CCTAAATA

01t445 145bp  
TCCTACTGAA GTGGCACCGG ATTTTGCTGT TGGGGGAATG CAAAAGGGTC AGGCTTCTTC  
ACTCTCTCCA TGAATCAGGG GTGGTAGGAA CAGAGGCAG  
C/T

GACTGCTGGG AATTGAACTC ACAGAAGAAA GCTGAATCAT GGCTC  
01T446 144bp  
GACATTTTAA AGGCAGCAA TTCAAAACTA TAACTCAGGA TAGACACTGA AACCATACTT  
C/T  
GCACCAGATT AAGAAAAGTG GCTGTTGGTA GTTATCAGTG AGATGGCTTC TTTTAGAAAA  
TTGTTGGCAA TGAAATAAT ACT

01T448 125bp  
ACTTGAAAAA TGTATTTCAA ACCTGCATAT TTCTCTGCAT CTCCACAGCC ACCACGCTAT  
TTAAGCC  
G/A

Table III

CTGTTATCAT CACCTGGACC ACTGTGGTTT TCTCTGTTCC CTAACGCACC TCTTTTC

01T450

CTTACCAGCA CTTGATATTC TGCGCTCTCT CTCCCATTCC AGCTGTTC

C/T

CTTTCTAACT GCTCTTGTG CTCCCTTTC TTGCCTCTCCC GTTCCAGTCT CTCCAGCCTC

01T454 144bp

CTAGACTCAA CTGGCTGGGT CACCGATGGC CATTTCATCT GTGCGTAGCT ATAGGGATTT  
AAATAGGAGG ATTTTGTGA AATGAAGACA ATTGACC

A/G

ACTGTGCGTG GAATCAATGT GCAGGATGAT TCACCAGGCT TTCTGC

01T455 147bp

CTCCTGACCT GAGGTGATCC GCTCACCTTG GCCTCCCAA GTGCTGGGAT TACAGGTGTG  
AGCCACACCG CACC

C/T

GGCCAATAAT ACATTTTAGT TCAAGATTAG TGAGAGCTAA GGAGAAATGA GAATGCTGAT  
TGTTCTGAAA TT

01T459 120bp

ACAAACAGAA GCTACATGAC AAGTTTTGCT CTGTTCAATT TTTCTCTTA AACTCTACTG TGT

A/G

CTGTTTGGA AACGCTATTA TTTCAGAAGG GAGAATCTCA TCTGGAATCA GAAGAT

01T462 149bp

CTGCAAAGTA GATATCTGA ACCCTCATTT TACATTTGTA GAACTGTAG TACAATTAAG  
TGATTTACCT TGGACCAC

C/T

TCACTATCAT TTGAATCCAA TTATATCTAG TTGCAAAGCC CACTCTTT CCACTACATC  
CTGGTAACTG

01T464 145bp

AGGTTAGAAA AGCAAACAAA GGTACAGTAT ATCTACAACA CCTTAAATTT GCCACTGAAG  
TTTAGATTTA CAAGTCAC

G/A

GAGTTTCACT TAATTTCTGC CTGAATATGT GTGAACACTC TTGGGCCATG AATGCCGAAC  
AAGGCT

01T465 137bp

TATTTGCAGT GTTTTCTGAC AAATATTTT CCTCCAGATT TTAAGC

A/G

TGTTATGATG AGTCAACCTT TATGTTTGTA AAGCCTTAGT CTTGTTAATA ATGTATAACT  
TCCAAATGAA TCATATACTT ATGCATAGCA

01T469 125bp

GCAGCAATTT TAGAACCGTT CTAATTTGAG CCAAGACATT GTCTTCATAT GCCCA

C/T

ATCTGCTAAT CAATGGATTC TGCATGCCGC TGGATGGAGC TATAACCTCC AGCAGGGCAG  
CTGCCTTTT

01T470 115bp

ATTTGAAATT CACAAGTGTG GGTATCAAAT ACACATAGGT GCTCTTAACT CAAGGATAAT T

A/G

AAGCATGAGC TCAGGCTCAG AGAGGCTAAG AGATTTGTCC AAGATCACAT AGC

01T471 133bp

Table III

TTCCTCCTCT CTTTAGCGCC TCCCTCTCCC TCTGCTATTG CTTGCCATGT TGGAACTGTC  
 AATCACGGGA TCCTCTCCCA CTTTCA  
 A/G  
 CAAGGGAGGG CAACTGACCC AAGCAAGGCC TCTCAGACTC CTCCTC

01T473 131bp  
 TTTTGAACCA CAGGCCTCAT AACTGAAAGT AGACTCACCT TTTTCAATAA TAGATGACAA  
 AATGTCGGAA TGTTTGCTTC C  
 A/G  
 AATATTTTAA TTTGGCATT TATCCTGAATC ACTTAATATC CCTGTGATG

01T474 143bp  
 CTGCCACACC TCTGTAGCCC AGAAAGGAAA TTTTCATATT TACTTCTTTA GAGAAACCAA  
 CTCCAGTCAT CTACAG  
 C/T  
 GCTTCTTTTC TTTCTGACCC TTGGAAAAA TGTTATTGTC CACGTTTTAG CTCATACTGC  
 TGGCCT

01T475 14 bp  
 CTAGAGAGGG CCTGACAACG AAGCTGTTGT GTCAGGGAAA TGAACAAGCA GAATTGTTTT  
 TTCATTGGGC  
 A/G  
 GGTAATGCAT TTATGTTTCT GAGGGAATGG ATACATCTTT CCGTTTATTT TTTAAGCAAG  
 TAAAACAAAC AAAACAA

01T477 107bp  
 CAGCCAGACC TGCCCTGACT ACAACCCCCA CACTTCTTTC CTGTGTGAGA AAG  
 C/T  
 AAGCCCTGGT TCTTCCGTT TCTATAGCAA TGTTTTCTGT TACGCGTAGC CAA

01T478 143bp  
 GCTGGATGGG ACCAGAAAGT GAATACGCCG AGGCATAGGG TTGTAGCAGA GAAAGAGGTT  
 TCATCGTAGG G  
 C/T  
 CACCGAAGGA GGAAATGGGA GGAAACGTCA AATCCATCTC CCTGAGGAGT TTGGGGCTGG  
 GGTTTTTTAAG G

01T479 106bp  
 AGAAGGGCGA GGAAGGACTC TTCCCTGGGG CTTTCAGAGG AAGCACAGCA C  
 G/A  
 GCCGACACCT TGATTTCAGA CTTGCAGTCT CCAGAACTAT GAGAATACAT TTTT

01T481 134bp  
 CCTGGGTCCA TGTGGATGGG CCTTGAGTTT GAGTCCATGG GGTTTAGCCT GGTGCT  
 A/G  
 GGGTGAGCCT GGAGCTTGAG TATGCAGAAA GAGACCTGGT TCTTGGGCCT GTGGGGACCT  
 GTCTGGATCT TGGGTCC

01T482 147bp  
 GTTTCCAGCA AACTGTGAC TGTACTTTTA CCAGAAGAAA TATATTAGTG TAACAGATGT  
 TGACTCTACT GTAGAAGCTG TGTG  
 C/T  
 TAAACCTAAC ACATGCCTAC CAAGTAAAG TAACTAGTTT TGCTGTTTTG TTTTCTCAGT  
 GC

01T485 148bp  
 AGTCATGACC TAAATTAAAC AGCATATTCA ACTTAACAAA TTCCTCTATA AACTT

Table III

C/T  
TATGGATCCA CTGAAAAATG GCCATCTGTT TCCTTTTATG AAGTCAAATC ACATCTAGAA  
AATGGCACAC ATACCGTAAG TGTTCCCTCA TT

17D143 not use Bsl1  
CTTCCTAACT CGGGGGGAGA ACGGGGCCAG GCCGCCCAGG GGCA  
G/A  
GAGCTTTAGA ATCAGGGTGA CCCCCACCCC TACTCCCCAA GCACAGTCAC

17D256 116bp  
CTCCCAAATG GATATTCATT CACTGCATTC ATCTTACCTT TTCTGAATGC A  
T/C  
CACATTTAAA GCCGCACTAT GGGGAGCCAC GGATACATAG TCACTGTCAT TAATCATCGT CACC

17D279 108bp  
TAGAGATGGA GTTTCACCGT GTTGCCAGG CTGGTCTTGA ACTCCTGGGC TGAGGTGAT  
C/T  
TGCCAGCCTC GGCCTCCGCC TCCTTTTTGT CCTTACATCT TTTATCGC

17D350 142bp  
GATCTAGCCT CTCTCCAAAC CCTTCTTTTG TTATAGAGTA TAAAATTCTA GAGTGAAAAC TAA  
A/G  
TTTCATGGCT CTGAAGACAT TTCCCTATTG TGTTTTTCATT ATACTGTACT TGAAACTATT  
GCCATTGTGT GATACATC

17D402 139bp  
ACTCCAGCCC GGGTGACAAA GTGAGACCCT GTCTTAAAAA CAAAAAAGAA AAAAAAAGA  
AACTTGTTGG CTCGATTTCA GTGTTCTTCA  
A/G  
ACTTTGGTTG GTTGACTGCA TGTACTATTG CGAGGGAAAA ACATTCCA

16\_001 125  
CCTCAGTGCA GCTCCTGGCT TACCCTCTTA CTGTGGGGGA TTTACAGGCT  
GGAG  
A/G  
TTGGGCGGCG ACCTTTCCAG AGCAGTCATC CCTCTGACAT GTTCAGGGAA  
TTTGCCAGG TCTGCCATGG

16\_002 139  
TGCTTTTTGT TTTCCCCAAG TGTGCAGCTG GTGCTGAGAG GTGATGGTGC  
TGCTTGTCCT CACACAGGAG GAGGAAGGTG AGGACGGCGA TCCATC  
A/G  
TCAGGGCCCC CAGGGCCGTG TCACAAGCTG CCTCCCGCCC CC

16\_003 106  
AGGGTTGGGC AGTGAGACGC GGCTGGACCG CAGCAAAGGA GATGC  
A/G  
CGGAGCGACA CAGTTCTGCT CGACTCCTCG GCCACACTCA TCACCAATGA  
GGGTAGGCTG

16\_004 127  
GGGCCACTTA GCGGGCAGA ACGCAGGGGC CAAGGAGCAC CACAGGAAGA  
TCCCAGCCCC GCTGGCGATG G  
G/A  
CACCTGCGTG CAGGCAGAGG GCAGCACATG GAACAGCAAC ACAGGCCTGC A  
ACAGG

16\_005 145

Table III

GTGCGTGTTG ATGAGTGGGT CGCACCAGGG TGGAGCCTCC TAGAAGGGCA GGGG  
C/T  
GCACCATCCT TGGGGAGTGG CCTGGAGAGG CCTCGGGAAG GGGGTCCAGG  
GTGGCTGAGC CTCAGCCATC ACCCCATGCC GTCCAGCCCT

16\_006 108  
GCACAGCCCA GCAGGGGGTC CTGGGCCTCG TCTGCCAAGC CTGCTGCATG CCTGG  
A/G  
AGAGGGGTCA GCTCTTGGGA CTCTGGAATC TTGAGAAGGC TGATCCCTGG TG

16\_008 147  
GGATGGCTGC AAAGTGCAGA CCGTCTGTGC ACGAGGGATG TGAAGAACA  
TCTCCCCAA GTTCAGAGCC AGTTCCAG  
G/A  
GTGCAGGCAC ACCCACGCAG AGCCCTGCCT CCCCTAAGGA GCCCCCGAG  
GTCAGCAGGG TCCAGGC

16\_010 115  
TGCGTTAACT TTTTCGCAGA CGGGAAACTG GGCAACAGGG AGGCTACAGG  
CCTTGCAGGA GGCCATCGGC  
A/G  
AGTCCGATGC TCAGAGCACA AACGCCTGGCC TAAGAGGTGG TGTC

16\_011 118  
AGGGTGGAAT TCTCTGTAA GTCCACCCTG CCCCAGGGTG CTCCTACCCT  
CTTGGTCTTT TTAAAG  
C/T  
CAAGGTGCGA TTTGGGCACC TGA CTGTCCA GTTTACCTTA ACAAGTTTGG  
GA

16\_012 145  
GTCTGAGTCT CGAGTATGTG ATTGGCCAGC ATCTTGGGGA CGGTGGTG  
A/G  
AGGAGAAGCA GATGTCCACA AAAGACAGGT TGCTGAGGAA GAAGTACATG  
GGGGTGTGCA GGCAGGAGTC TATGCTTACG GACAGGATGA TGAGCA

16\_013 96  
CCCTTCTCCT CCCAGCCGGA CCAGACTCTG CGCACCAGG TGTGGGCT  
C/T  
CCTCTGTGCC GGGGTGTCTC CACTCGACTC TGTGATGTT TGGGATG

16\_014 135  
ACATTCTGTG GACTTGGACA AATGTATAAT GATGTGCATC ATT  
A/G  
TAGTGT CATG CAGAGTATTT TCACTGCCCT AAAAGCCGTC TGTGTTTCAC  
CTCTTCATCC CTCTCTCCTT CCCAAAACCC TGGCAACCAC T

16\_016 149  
CATCACCTTC CAGAGCTGGA GGGGACGGCC ACCCATACCA AGGTCCTTTA  
GCTGACACCT AAACCTCAGGA GCTAACCATG TG  
C/T  
AGGTCACACA GGCCGAATCA CAGCAGTGAT GAGACGCTGG GGTCTCCACA  
CAGGAACCCA ACTGAC

16\_017 123  
AAACCCAAGA CAGCTGAAGC GGGCTGTGCG TTTGTCCCCC AGCTAGGCCC  
AGGGAGTGGG CATCTGG

Table III

A/G

ACGCAGGATC TCCTGTCCTC CCGACACCTC ATTACCCATA TATGGGCACC  
AGCCT

16\_018 115  
TAATCCAAAC AAACCTAGAGG CTAATTGCCA TTCCCCAGCA CAAAGCTGCA  
GTGACGATGA TTCTTTAATT C  
C/T  
TTCTACGTGC TCACAGCCCCA CGGCGCTCTA CTCTGCTCAC TAA

16\_020 117  
TACCTGCACC AGCCCATTTCT AGACCTGGCT CTCTTTCCAG GCCAGG  
C/T  
GGGAGCTCCC GAGAGGGGTC TAGGCATCCC TGAAGTCCAG GCCTGTACTA  
TTAAGCAGCT CATCCTGGTT

16\_021 132  
TCAGAGAAGC CTTATGCCGC TCGATTTCCC ACCAGCTCTG GAGTCGGGTC  
CTCTCCACTT CCACACATTC  
A/G  
TTTCCACAAG ACAGGTCACC TTTCCACCAG TGTGGACGTC TCACAGTAGA  
ATCAAGGACA A

16\_022 98  
GGAAATGCATG TTTCCCCAAA CATGTACTCT CGGAGGTCAT ATTAGTCT  
C/T  
TTGCTTCCCT GCTCTTTTGT GACAAGCAAT GTTAGGATAG CAGTGGATG

16\_023 128  
TCTCTCCTTC TGAATTTCTGC GATGGGCCCG GGAATTTGGT TTACATAAGC  
AGCCCCGTTT CTCAGACCCT  
C/T  
TGTATCTTCT TCTGGAGTAT ATGAAGGCTG TGGTACCAGG CCAAATTTTG  
CACACAA

16\_024 121  
AGCCGGGTCC CTTCTCATC AGTCACCATT TAATGGAGAC TGAATGGTTG TGGATAC  
C/T  
TTTGTTAGGG TCATCAAGAA GGTGTGCCAT GCTTGGCTTG GTAAGGAGGA  
GGTTGTGTGC TCC

16\_025 89  
ATCTTGTCTT CCTGTCACAC CCACCTGGCA CCACCTTCCA CCCAGCT  
C/T  
TGAGTCAATC CACCACTTCC TCACCTGTCA ACCACCAAGC CTCATTAC

16\_026 105  
TCTCCACATT AGGGCAAAGT GAGCTCACAT CTCTCTTACC TGCTCTCTGG  
GCCTCCC  
A/G  
GCCTGGACTC GCACAAGGGC ACCATCCCAC TACCCCTCAT ACTTCCA

16\_028 92  
TGCCCCACGG GCCTTACCTA GTCCCCGAGA ACTTCCGGGA GAG  
A/G  
AACCTTCAGC TCATCCAGTC CATCAGGGAC TTCCTGCAGA GCGACGAG

Table III



16\_031 136  
 TCCCTCCTA ATGTGTCAAT GGCTTTGCCA GGAATTGCAT CGGTGGTGTG TCAGG  
 C/T  
 GGGCTGTTGT CTGGTTTCTG TGACAGAGAC CCTGAGCAAC ACTGGTTTAG  
 ACAAGGTAGA ATTTTCTTTC TTCCCACTTG

16\_032 149  
 TGAGGCAGTT CTGTGAAATC CTCTGCATGG GCTTTTGAAA TTCCAAGGTT  
 CTCTTCTTAA GGGCAGG  
 C/T  
 TGCACAGTAA TTTCCCGAGG AAGGCTTTGT TCCATAAACC CAGGCCTTAC  
 AAACAACAGT TTCCGCCTCT GATATGTATA A

16\_033 141  
 GCATTACTCT AGAATTGGCA TCAACCCCAA GCAAGGGAGC AGGGCTTTCA  
 TTCTTATGTG CCTA  
 C/T  
 GAGTCGAGTC ATTACCAAAA GAGATGGAAA CTTCTAGCTA CTCTGGCTCA  
 TTGCATGTTG AGGGAAAATT TCTCCA

16\_035 120  
 CACGCTCAAC AGCTGTTCCC CTAGCTGTAT CAAGTCCAGG CCAGTGAGCT  
 TGCTTCTCTC C  
 A/G  
 GCTTGTCTCA GCAATTTTGT TTTCCCCAC TGCACAAGTT CCTAACAGCT  
 CCAACGAG

16\_037 147  
 ATGGGCGCAT GGGCTCTTTT ACAAATGTGC CGTGGTCCGT GCATTGTGCT  
 GCTGTTGTGC CCCTCTGCTG CAA  
 C/T  
 GGCAAGGAAG TCCCTTTGCC TTGCGTACAT GGAAGTTGGG TGCCAGGCTC  
 CCAAAGCAGT TCTTCTTGTG CCC

16\_038 127  
 ACTCCCCCAA ATCTGGGTTT GAATCCCAGC TCCACCACTG CAAGTCTGGT  
 TGCTCTGGA  
 T/C  
 CAGTTACTTA ACGTTCTCTA AATGTCAGTT ACATCCGTGA GATAAGCTAC  
 CTCGCGGGAC TTCATTC

16\_039 111  
 TTGCCCCCTCT GGAGTTTACA GTTCGGGGGC AGAGACAATG AATAATGAG  
 A/G  
 CAGATAAGTA AATAACGGTT TCAGATAATA CTAAGGGCAA TGAAGAAAAT  
 AGTACAGGTG A

16\_040 143  
 CATCTACAGG GTTCCTTCGG GCTATGTTTC TAGGGTGAAT GGCTGAGATA  
 TAAGTGATGT GCTAT  
 C/T  
 CAAGGCCTTT GATCGGTAGT GGGGGAGACT CGGGGCAGGA GATGTTTTTG  
 GCGTACCCTG AGACACCATC ACATCAT

16\_041  
 GGGTTGCCGT TCTAATTAAT CTCTTATCAG TGCAGTCAGG GGTCTCCTTT

Table III

GGAGCCTCTT GTGGGGGTCC CACTTCAGTA GTTACTAGAG CAGCTTT  
 C/T  
 TGTTACAGAG GTCCCCTTTT GAGTAGGTTT ATAAGGAATG TGAGAATT

16\_043 124  
 CACACTGAGG CAGCACCTCC GGGGAAGTCT CCGTGCTCCG ATGCTGTGGC C  
 A/G  
 TGTACAGCAT ATGCAGTCCC CAAAGGGATA TTTCAGCACA GAGTTTCAAT  
 GTAAAATGAC ACACGCTACT GC

16\_044 135  
 GCATAATCCT TAGCACTTGA AGACTTTTTTC AGCACCAAGG ACAGCAAAAC  
 GTCATCGTAA TCAGCACCCA  
 C/T  
 AAGCATCCAC CTTAGGATTG CCTAGGGGCC GGCCGCTCTC ATAAATACAT  
 AAAGGGGAGG AAGG

16\_045 138  
 AGGGCGGCCT CTCCTGCAGC ACGAGGCCTA CCTGAGGGGC AGTAGGAGGA  
 TGAGTTGGGC ATTCTCC  
 A/G  
 CGAGAAGCTC TTGACCACCA GGCTCTGGCC CCACTGCTTG CGCCGCCACG  
 CCGTGCGGCA CTTGGAGTCG

16\_046 137  
 TCCAGCTAC TTGGGAGGCT AAGACAGGAG AATCGCTTGA ACCTGGGAGA C  
 A/G  
 GAGTTTGAG TGAGCCGAGA GTGCGCCATT GCACTCCAGC CTGGGCAACA  
 AGAGTGAAAC TCCATCTCGA AATTAAAAA AGAGT

16\_047 106  
 GGTGAGGAGC CTGGAGCCCC ACGCTGGGCC CGAAGGTTCA AGGGCTTCTC ATCAG  
 C/T  
 GGCTTCTCAT CCGTCTCACC CTGGTCTGCG GCTTCTTCTC TAAATGCATT

16\_048 111  
 AGCTACTGGA TGCCTGGGT CCGCCAATCT CCAGGGAAGG GGCTGGTGTG  
 A/G  
 GTCTCACGTA TTAATAGTGA TGGGAGTAGC ACAAGCTACG CAGACTCCAT  
 GAAGGGCCAA

16\_050 133  
 ATCAATTTGC TGCTGTTTAG TAAGGTATAA ACTACAGTTA AGGTTAAAGA  
 CCTTGCCACA TTCTTTCCAT TTA  
 C/T  
 AGGGTTTCTC TTCGGTAGGA ATGATCTGAT GTTGAGTAAG GTGCAAACTA  
 TGGTTTAAG

16\_051 145  
 TGATCTCTCC AAGGACTGGC CTGGAAGGGA CAGAGAAATG CGAATGCCCT  
 TT  
 A/G  
 AAATACTCA CAGCGTATAG TTGAGTGGTT TCCAAAGACC CCCTCTATGC  
 TGCCAAGCCC TAAGCATGCT CTCGTATCTG TTGTTGGGAG AT

16\_052 98  
 AAATGCCCAG GGGTTGGCAT GAAAGACCCC CACACCCTGC TGCCTGCTGC

Table III

A/G

GGAATTGACC AGGGCATAGG CTTAGAGGGG CCTCATCAAT AATAACC

16\_053 125

CTCTCCCCAC TAGGACAGGC ACGTGTCTC ACTAGGACAG GCACGTGTC

T/C

TCATTGTGTG TAGGTCAACA TGGAACTTTC TCCTACTGCT TGCTTTGGTA

AGAATGATGG GTTATCGGGA GGCTG

16\_054 116

CATCTTGATG CACCAGGGTG GTCCTAATGT TCTCAGATAC ATTAGAATCA CACAAT

A/G

TGGTCCCTAA ATGAGAGCCA ATTCTGTCTT GTCATCAACC AGAGAAACAG

CAACTTGTT

16\_055 113

CCTTGCA GTT CCGAGAGATG GTTAGGGAAG AGGGACTCCC AGTCAGCAAC A

A/G

TGCGATCTTG TAGTAAATGC CAGTCTCAGC TCCAGGTTTG GTTTGACCCC

ACATGTGTTG G

16\_056 131

TGAGGGTTCT GTGCTTTTCT TGCTCCAATG CTGAAGAATG GCCTGCTGCT

TTCCCAGGTG TCACGGGCAC TGAGAAAGGG CCCC

G/A

TGGCACCAGG AGCTAATCCT CAGGGGTCAG AGGCTGTGGG AGATTC

16\_057 139

CTGGGCTCCA TCCTCCCTCT GGCCTCACCT CCCCAGCCAG CCCAGG

C/T

TGCGCCAGCA TCTTCTTCCT CGTCCACACC CTGCCCTGCC ACTTCGCTCT

CCTTCTCTCT TGGTCCCTGC CCCGTTTCTA GCATGCCCC TT

16\_058 143

CTTAGCCTCA GAGGTGTGCA TCTACTCACA GAAGGGCTCA GTGGCTTCCA

GTGTTCAAGG TTAGTGATT GCACA

G/A

GAGCTGTTAT AGGACAAGCC CCGTGGATAC TGGTGGCTCA GAGGTCTTAC

AGATGAGGTT TCACTGG

16\_059 138

GCTTTCTGTG TGA TAGTCT TCTAACTGCT GTATAGACCT CCAGGCTTTG CCT

C/T

TCCATCCTGC CAGTGACACC AGGACTGCTG CCACCATTCA TGCTGTGCGG

ATCATTATCA TCCATGTCAC CTTTAGGGCC CACT

16\_060 117

CGGCCAACT TAAATTTTAA AAAGAGGAAC AGAAGTCAGC CAGACCAACA

AAAGAGCGAC

C/T

GGTGTTCCTA GCATAGGAAA CAGAGGAAAC AGAGGCCAAA ACCTCGGGAC

TGTGGA

16\_061 125

GAGCCAATGG CCAAGAAACA GTTAATAAAA TAACAGACGA TGGTCCTGGC

CTCTACTGTG AGTGAGTAAA G

A/G

Table III

GCTTGCCCTG CAGAGATTCA GTGATCTGGC GGGGGTTGCT GAGCTATGAG  
GAA

16\_062 100  
ACTCTTCTTT CTTGTCCCTC TCATCTAGGC ATGGCCATGC CTCTTCAT  
C/T  
GACTCCTGTG TGTCCCTCC CCATTCTTGC TGTCAGACAG CGTGCTGGTT  
C

16\_063 140  
ACTTACAAGT CTGGGGTCCG GGGCTCCCCG GAGCTGGAAG ACCAAGGCCC  
CTGTGCCTGG GATCGCTGGG TTA  
G/A  
GGGCGGGTTA ACCTAGGGGT CCCAGCCTCC AAGTCTGGGG AGGATCCGGG  
TTCACGGGGT CGGAGT

16\_064 119  
ATAAGTGAAT TCCGCTACGA TGGCCAACCT CTGCCAAACC CAACCTGACC  
AGTGGCCAAC CTGAGCATCA CG  
G/A  
TGTTTCAGCCC ACTGATGGCT GCCTCCAGAT GCTCCCTGAA GGGACA

16\_065 141  
TTCTCTGCTA AAATATTGCC GTCTCAGTGA ATCAGCTCTA GATGAACTCA  
TTGGGTGATT GTAGGAGAAG CCCCTCCCTT TGGGGCTTGG AGAACC  
C/T  
TGGGAAGGAG AAAGGACAGG TGGTGGGGAG AGGTGGGTTT CCCT

16\_066 112  
GTGACTGTTT CAGAAGCTGC CTACTCTTCT AGTGCCTGCA GCAATC  
C/T  
GAGGTGTGGA GGGCACTCCC ATTTCCCTTC CCTGTGCTTG AGAATCTGTA  
GAAATTGTGC AACTT

16\_067 119  
CCACTCTTTC CTCTGGCTTC AAGTCACAGT GTGCCAGCAT CCACATGGGT  
AACTCAGGGA TGATG  
A/G  
AGCTGGTCCC TGACAGGGCC TCACACCTCT CGCTGGTGGG CACTGACCTA  
TCC

16\_068 123  
ACCAGCTTTT CCCCAGGGGC TTAGCCCAGG GCCTTTCCGG CACCCAGAT  
C/T  
GCATCTTCTT AGCTGTGCCC CAGAGAATGA GGTGAGATT GTGATCTGAA  
ATATTTTCAA GGCAGGTGCT GCT

16\_069 113  
CCAATAGCAC TGTGCTTGAA TATTAGATCA AGAAATGGCC TGACAGCCCA  
AGACCCCTTC TCA  
A/G  
TGAAATTAGC TTGAGACTTC TGACAAGAAC GAAAGTATTC TGCCCAATG

16\_070 106  
CCTCCAAGCC TCTGCACCTT CTGTTTCTTG TGCTCAGGCT TCCCTCCACC  
TCCCACCC  
C/T

Table III

TTTGTCTCA TGGTTGATGC TTCTTCTCCT ATGCCATGTA TTCCATG

16\_071 115  
 ACACATCATAT CCACCTTTAT CCTAAGTCCC CAGACCTAAC TAATGCCTTC  
 TCAGT  
 G/A  
 TCACCCAAAG CCTAGGTCTT CCCTTATTCC ATGGGATAAC TGCACACAAA  
 ACCAGGATC

16\_072 122  
 ACATGTTTCC TCTCCCACTT AGTTGGGGCC AGGCCCTGGG GAAGAGAGTT  
 TGCAAGAGGC CCAGGTTTAG  
 C/T  
 TGAACACGTG GAACCATTGG TGAGCTCCTA GCTCCTGCAG TCCTCTTTCC  
 A

16\_073 138  
 ACTGCAGCTG CAGAATGACA GAGGCCATGT CCAAATCCC TTAGAGACAC TG  
 C/T  
 TGTCTTAGAG TTGTTAAAT AAGAGCCCC ATATCAGGTT TAGAAAATAC  
 TGTCACCGAA CGAACGTCGC TGCTCTCAGC TCCAC

16\_075 100  
 TTTTAAGCCA CTGAGTTTGT GGTAATCTGA GGACCCTGGT GTATG  
 A/G  
 CAGATGCAAT TGACAGCAAT AACAACTTAA GCATACCCTG TATGGCAGAC  
 ACAC

16\_076 143  
 TGACTCGGGC TGGGTGTGGA TTCTCACCCC AGGCCTCTGC CTGCTTTCTC  
 AGACCCTCAT CTGTCACCC  
 C/T  
 CACGCTGAAC CCAGCTGCCA CCCCCAGAAG CCCATCAGAC TGCCCCCAGC  
 ACACGGAATG GATTTCTGAG AAA

16\_077 146  
 CTTGGGGGAA GGTGTCATGA TTGAACACAG AACTTAGATC TGAGCTTCCT  
 GGCAGC  
 C/T  
 GATGGAAAAA GGCAAATCA GTGAGCGCAT GGCTCACATT CACTCCTAAA  
 AGGCAGCACA GATGAGATCG TAAGGCAAAT GGCTCTGCA

16\_079 145  
 TATGAAGATG AAATCAGCGA TTCCAAAGCA CAGCTAGCTG CCATCACCTT  
 GATCATTGGC ACTTTTGAAA GGATGAAGTG CTTAGTGAA GAGAATCA  
 C/T  
 GAACCTCTGA GGAATCAGTG TGCCCTTGCT GCATCCAAAC TTCTAA

16\_080 145  
 ATCAAAAGCC CATAGCAAAT TCTGTTCTGT TCTTGGGGAA GCTGACAGTC  
 TGATTGGAG GCAGAGGACC CCAAATACAG GCAGCCTTCA CC  
 A/G  
 ACCCTGACTC AGGCAGTGAT ACTGCTGATG AATCTGTGGT TCCTGCCGGG  
 AG

16\_081 121  
 AGCGTCTAGC ACCTGGTACA AACCGATGGC ATCTCCAGG CATTTCTGAA  
 CCATTTTCAC.

Table III

A/G  
 TGCTCTACT CTCCGGCCGT CTCCACACCA CCCTGTGTTT TGCCAAAGGG  
 AGCTAAAATG

16\_082 144  
 AAATTCAGGG TTTTCACAAA CGTAGTGAAT TTTCAGCTTG TAATTTGCTG  
 TCTCCGGTGA GCG  
 C/T  
 GGTGCTGAGA AGACCCGTGA TGCTCTCTTT GAAGCCCATT TGCGGCATGC  
 CCCAGGCCTG GGACCTCCAT TAAGCACCAG

16\_085 131  
 AGGAATTCAG AGCTGAAAAT GACAGGAGAG CTCCTCTGGC CATTTTACGG  
 ATGAA  
 A/G  
 CTAGAAAGAG CAAGATATTG TCCAATCTTA CAGGGGAAAT GAGCAGAGCC  
 AGGAATCTCA GGCTTGGAGC TGGGC

16\_086 149  
 TTGAGCCTGG GGGGTCCCCT CGCCAGCACA AGCGCCGGTT GGCAGCAGGG  
 CTGGGGCTTT CCCTGAGGAA GGGGAGGAGG TAGCCCTGCA TGTGAC  
 A/G  
 GCGTGGGACA GTCCAGGCTG CACCTCCTCT CTCCAAGAGT GTGTCTGCAG  
 GT

16\_087 145  
 GCAAGGGAAA AGATGTATCA ATTTTCTCTA TAAATGAAGA GGCTGTTGCA  
 TGGATCTGAG AAAGCCATGG GGTGAAAGGG GACAGGCCTC C  
 C/T  
 TAATGTTGAG TGACAGAGAG AACTGCAGTG GTAATCGTTA ACCAAACCAC  
 CTG

16\_088 149  
 AGTCCGAGGG ATGTAGGTGA CAGGGAGGCT GCTCAGCTCA GCCCTGCCTG  
 CCTGC  
 A/G  
 CCACCCAGGC TCCCCAGGG AGGTCCAATC TCCCACCCAA GGCAGGACAA  
 GGCAGACGAG AGCCTCACGA CACCGACAGT GACGCACACT TCC

16\_089 139  
 CATGACACTG AGTGAGGGGC CCCTTAAGGG CTATGGGTAC AGGTAGG  
 A/G  
 ATGCTAGTTG TGGCGAAGAA AGCTAGAGCT GATTAATTAT GCAGGCAGCC  
 CCACCTCTGC AAACCACCCA TCTGGGAGGT CAGCCTGCAA A

16\_090 124  
 GGATGGGGGA GGTGGCCCTT AATTCTGCCT TGAGAAACCC CGCCTGAGGC  
 CTCAGCACCT CCTTGTCCAG CCACCCACA  
 A/G  
 GTGAGGGTCA ACTCAAGTGC CTGAGTGTCC TCTCTGCACC CTGA

16\_091 136  
 TTTGGGGCAG CCAACCTGGC ACAGCTAATC AAAGACTGAC ATGGAAGCCA  
 CTCCCTCTCC CCTCCCCTGT ATCACTGACA CCATTTTCC  
 A/G  
 TCGTCTTGTC ATCGCAGACT TTACAGTTGT TGTCATGAGT CTAATC

Table III

16\_092 108  
 GTTCATGTGT CAATTACCTG GTTACTTAGT AACCAAGTAA TCCAGTAACC  
 AAGAAGTCAA GCC  
 A/G  
 TAGATTAAAT AGTCCCCAAC CGGGCAATAA AAAGGTCCCT GAGTACAAAT  
 TTGC

16\_093 85  
 CTACAACCCT CAAATTCAAG TGACAGAGCT GGGATTTTGC AC  
 A/G  
 TGCACATCCA TCAGTTATTG AATAAGGCTG CTCTGAAAAG GG

16\_094 149  
 ATCCAAGAAA TTAGACACAG CCCTAAGAGA AACATGCAGA AATGAGCAGA  
 ATAGACCCCA AATAGATCAA AATTCTGTCC CACCCTCTGC C  
 A/G  
 TCCCTCTCAG AATGGAAAGT CAACAGCAAA ATTAAGTTTG GTGGTGAAAA  
 AATAACT

16\_095 119  
 AAGGGAAAGG AAGAACATAT GGGGAAGGCC AGAGTGGAGA CAGGCAAACC  
 AGAGCCTGAA AACGAAGC  
 A/G  
 TCCTCTAGGT TAAGTTGAGA GTGTAAACTT TAATCAGAAG GCAACAGAAC

16\_096 137  
 TGCCCTCCAG CCTGGGCTCA GGTGACTCAA GGGAGAAAGC ACCT  
 C/T  
 CCTCTCCCCG CCAGGGAGGT CTCGCCATGT TTTGGAATCA GTACCATTCC  
 CTTGGGGCTG GGGGGCAGCC CCCATCTCTG GACCTGGCTG GA

16\_097 126  
 AAGTTGTAGA TGGCCAGCTG GTACCATGGA GTCTAATGAT GCCTCATCTG  
 TCCAGTGCTG ATCTTCGACA TTCCC  
 A/G  
 TGTCTGGGAT GGGAAATCCA TTTTGTAGAA CGAAAGGAGA CAGAAGGCAA

16\_098 130  
 AGATGTGTGG TCATTATCAC ACCGTTTGGT TTAATATTTA GCCAATGTCT  
 TGGTCAGGGA GCCTCGTACA ATGGCTCTCC ACAATCCA  
 A/G  
 CACTACGATG ACATGTCTTT CTAACCTTCC AAACCACACT G

16\_099 137  
 GGAGAAAGAA AAAAAAACC TCAATTTCCC AGTGAGCTCA CTGCTTGCCT  
 CTCTTTCGAA GTTCCAAATT GCCT  
 C/T  
 CACTTTCTCA GAATTCCAAT CAGGGCTCCT TCAGAGGAAG CAATTTCTGC  
 CAGCACATGG TC

16\_100 148  
 ATTTAGGATT CCTTTGTTCT TGGAAAAGAC AGTGGCCTGA TTTTAGGAGC  
 A/G  
 GCATTTCCCTG CTGCCCAGCC TGCCATTTCT ATCACAATGG TAGTCAGTGA  
 GGGTGAATGT AACATTGCCG TGACTGTGAA CAGGAGGTAG CCCCATG

16\_101 133

Table III

CACAGGTTTT GCCTGTTTTG CTCTCAGATG TGCTCTAGCT CATAAGACAG C  
A/G  
TCAGGCATAC AGTAGATGCT CAGTAAATAG TTGCCAGTTG TGTGAATGTA  
GAACCATACA TCACCACAAT GCTGTACTAA T

16\_102 133  
GCTGTGTCTG CCGAGCCCAG CGTCCTCACA CAGCCCTGCT GCCACCCAGC CA  
C/T  
GCTGGCCAC ACGTCCCTTA GACAGCCGGC CACCTCCCGT CCCACCCCTG  
CTGCTTGTTT TGTGCCCTCA CAGGTTTGCA

16\_103 144  
CACTCCTGGA TTTATGTGAC TCCCTTAGCT ATACTTTCCC AGCCCCCTGG  
GATGTTCCCC ACTCATCCTA TTCAC  
T/C  
CACAAAGAAA TATTGTCAA ATCAATTGGG TGATGATTAG GAGCCATTAT  
CTGCCTGCTG TGCTGAAA

16\_104 139  
CACCTTGCTC TCATCTTTTT ACTCCTTTAA TGCTGACCTC TGCCAAATTG  
AATGAT  
A/G  
TATTTTCACA TCCTGACAAA AGGAACTGAC CATAGCTGAT AGAGCCCCAC  
ACCTCCTTAA AGAAAATGTT TTGTGAAAGC TA

16\_105 128  
ATGAAAGCTG GGTGGTCTTT GGGTAAGGAC AGGGGAAC TA GGAGGTAGGG  
TGCAGGTAA TGATTTGCTA CCC  
C/T  
TCTTTCTGGT AATACCACCA CCCTCCCTTC CTAGTTTCTT AGGAGGCCCT  
TGAT

16\_106 100  
TCTCCTGGGG AAGAAGGAAA CTAACCTCTT CCTATCCCC TATTTAATGC T  
A/G  
GCATCTGCTG TCCTCTGCTG TGGTAACAGG GAACTATCTC CCAAGGAG

16\_107 141  
TGTGGGGCAG CTGGAATCGG GCAGACCTGA GTGTAACTC AAGTTGGCCA  
CTGC  
C/T  
GGCTGTGCTG CTTCAGGCGA TTCTGTTGAC CTTTCTGTGC TACATAATGA  
AAATTCTTAT TTTACTGAGT GCAGGGGCTG GGCGGG

16\_108 107  
GCCTCAATGA ACGACATCAG CGCTTCTCTA GTTGGTGAGA AGGCCAGGA  
AAGCTTGGTC TG  
T/C  
GTCATACACT CAATAGCTTC TCCTACCCAG CCACCTACCC TGCC

16\_109 137  
TACTTGCTG GCTGCTCATG GTTAACAGAA GCCCAGGGAG AAGCTGACTC TA  
C/T  
CTTCTCTTCA GCCACACCCA AGATATTGGT ATAAGGGAGG CTGGCACCAT  
GAGTATTAGT ATAAGGGAGG CTTCCGGGTT GTGC

16\_110 142

Table III



GAACCCTATT GTGAAGTGTG CACGCAAGGG AACTAGGCTG TGCTCCTTA  
C/T  
GAGAATCGAA TGCCTGATGA TGGGAGGTGG AGCTGAGTTG CTGATGCTAG  
TGCTGAGAGT GGCTGCAAAT ACGGATTAAC ATTAGCAGAG AG

16\_111 121  
CTACTGGGTT TACATTGGAG ACCGTCCCAT TTAATTTCCA GGGTG  
A/G  
TGGGACAAAA TGGGCTCAGT TCTTACATAG CACACTACAC ATGTTTAA  
ATACAAAAT TACATTGTTG CTCCC

16\_112 109  
TCATCATGGT GATGGCATGC ACCTTTTTC GGGCCGGAGC CAGTTCTTGG  
AGGAGACTCT GC  
A/G  
CAGGGCATGG ATCACTGTGG TGCCCTTTTC CTGTGCCTGT GCCTTC

16\_113 108  
TTTACATTCT CTACCCTGTC ACACAATATT TCACAAGGGA ACCTGGACAA  
AGGGAAT  
C/T  
GGTGGCAGAA GGATGCTACC CTGCTCTT ATGAGCTCCC ATCACTTCA

16\_114 139  
GTCTCCTCAG TGACCATAAT GCTGAACAGT TGAGTTTCT CATTGTCCCC  
TATTA  
C/T  
ATCCTTCACC TCACAACTCT GTGGGAAGAG CAGCTGCAGG GTGCACTGAA  
TATTAATCTC AAAGCAGCAG GCTGATCAGG GAA

16\_115 128  
TGAAAGTCTT TCCTGGGTGT CCTATAATGC AGAGAGCCAA AATGATCCTG  
AAGAAGT  
A/G  
TCTGTCCCCA TGCTCATCC ATAGCATCTG CCAGGCCTCA CTGAACCAGC  
AGAATCTAGA CCTCAGTCTT

16\_116 129  
ACCCACTGCG TTCTGTTTTT TAGTCATCTA ACATACTTTG CAGACTTCTA  
GTCCCATCGA TACAGAA  
A/G  
GGAGTCTACA AAAGAGTAAA TGTGAACCTG AGAGAAAAGT GTCCCCATCT  
GGCACAGATA A

16\_117 123  
CAGCTAGACA CCATAACCTG GCTCACTGTC TGGCCTTCAA GTTCACTCA  
GCAGA  
C/T  
AAATGCACCC TTAAGTAACC TGGTAGGGAA CCTGTCACTC TACATAAAGA  
ATGTATGGCA TGCCACA

16\_118 141  
ATCGGCGGTG CTGAGCCGTG AGGTCCCCTA CCTGCCCTGT CAGGCAAAT  
A/G  
CTTGTGTGAG CATACTTCTT TCATCCGTCA CTCAGCCAGA GTCTGTAAGA  
CAGACTCAGC ACTAGGTCAC ATTTTGAAAG AGAAAATAGA

16\_119 105

Table III

GAAGATTTTT CTTCTCCTC CCCCTGTGAC CAATAGCCAA AGACATATTT  
TGGGATG  
C/T  
ATTAGTGCAC TGGGACCTTA CTCAGTCTAT AGATGACCAA GTTCACA

16\_120 133  
AAAGGAGAAA TACCAGTATC CGTCTTAAGA GCTGCTCTGA CAGCAACTCA  
CAGTTCTGAT AAACACTATT TAAGTGCCTT GTGAA  
A/G  
GCCTTTTTTG GGGAGGCTGT CAGCGAAGCA AGTGAGACCA TGTGATG

16\_121 145  
CAGTAAATCC AGGGCAGATG TATGAGGTAA TGAAAGAAAA TTTAAGAATG  
CACTCACACA TTGATGTGAG AACTATTAAG ATCCCCTTCT CTCTCT  
T/C  
CTATACCTCA AGTTCGTTAT CATGCACTCC AAGCTACCAA ATATTCCA

16\_122 141  
CGGGGACAAA TTATTCACCA ATCTTCATCC CAGGCTCAGA GGAAGATTAT A  
T/C  
ATCCAAGTTT TCCACTATAA TTAGGTTGGA GCCATATGAC TAGGCTCTGG  
ACAAAAGGAC AGTGGAATA CTAGGCATCA CTTTtaggc

16\_123 130  
TAGACAAAAG GATGAGATCT TGGTGTGGGG GGTAAAGGA TGAAGCTTTT  
TCGATTCTTC TAGCATC  
A/G  
TGCTAGACAA ATTCCAGAAA CAACTGGAT GCTTATGATG GAAGCAGCAG  
AGGCAAAAGA GG

16\_124 127  
GCTGGAATTA CACTGTGATG AACTAGGTTC CCACACTATT TGGTGGGAGT  
GAATGAGAGG CTTTGGATGT GAATGT  
A/G  
GGTGTGCCTT GTTCACCTTG CTCAGGTTCC AGCAGGTGCT CAATAAATGT

16\_125 119  
CTCAAGTGCA CATGAAAACC TTAAAGTCAT TACAGAATTG CTAGTCCACA T  
T/C  
TAGCCTCACA GTTAAATTTA ATAGTTCATT TGTGAAATTA ACAGACGAAT  
TTGTCTCGCC TGCTAGA

16\_126 105  
ATACCATAGC CACCCCCGAC ACCACCACCA GATTCCAAG ACCCCGGACC  
CAGCACCC  
T/C  
GAAGGGTCTC TGATTCTGCA CTGGAGCAGT TTCTTCTCCC AGGCCC

16\_127 136  
CTACTGAATC AGAAACTCTG GCAGTGGATT TCAGTCCTCC AGGTGACTCT  
AATGCAC  
A/G  
CTCAGGTTTG AGAAAGGATC CCTGCCCTA ATCCATCAAG CCAGGCCAGG  
AGAGTGCAAT CGTAGAGTCC ATGTGTCC

16\_128 139  
GTTTCGTTGTG TCTGGTACTC ACTCTGTGTG CTGCATCTCA CTTTCATCAT

Table III

C/T

ATGACAAGGT GTGCAGACAA GGAAGAATGT TCCTCTGGGC TGCTTACTGA  
TAAGAATCAC ACAGTGTAAG CCTTTCAAGG GAACTTAGA

16\_129 131

TTGCTATCAT GTAGCTAGAG TCGATTAAGT GGCCAAGGGT CCAAGAGACA  
GGTGAGACCA TGAGGAGGCA CATT

C/T

GATGTGATGT GACCACAGAA CCCTGGGTAG TCTCAAGGGT AGAAGCCCTG  
ATGATG

16\_130 119

GCGGGCCATT TCATTGGCCT ACTTTTCAA CATCGGCTAG AAAGGCCTTC  
AAAG

A/G

AGGCTTTGAA AACCAGCCGG CCATCTTCAC AATAAGCTCA GACGGTTAAA  
AGCCACGCTC TGGA

16\_131 142

GCTTGGATTT ACTGTGTTCA TTTCTCTGAA GCTTTTAGA AATACCTGAG  
GAGG

C/T

TGGGCACGGT GGCTCACGCC TGTAATCCCA GCATTTTGGG AGGCCGAGGT  
GGTCGGATCA CCTGAGGTTG GGAGTTCGAG ACCAGCC

16\_132 144

TTCCAGATT TTGTCTGGAT TCTGCCTGCT AGAGTGCCTC ACCTTCATGA CC  
A/G

GCTGTCACCC TTCATTCAAT TGAATGCCAC AGCTCTCTCC CCACACCCAG  
GCCTTTCTTC AGTCTCCTCA TGTCAATTCT CCTCCCAGGG A

16\_133 122

AGACCCAGGT GATTTTCATA GGTATTTCAA AGGCAAAGCC AGCTCTGGA  
A/G

ATCAAAGCCC TGCCCATCCT TCTAGGACTA GGAGAACAAG TTATTTCCAG  
ATTTCAAAAC ACACATGAGT GT

16\_135 138

TGGCTGGCCT GAATATATCT GGTTCGTGC GGACAGACTC TCTTTGGCTC  
ATGTATACCT TCAATTGCAT AAGGGAGAGA ATATAGAGGA C

A/G

TTCCAAAGGA AGTGCTGACA GACTGCGCCC ACCTTG TGAA GGCCAA

16\_136 129

ACTGTTCCAT GGGAGAGTAT TTTAGAGACG ATGGCAAATA TACTTTG  
A/G

TCATCTATGA CGACTTATCC AAACAGGCTG TCGCTTACTG TCAGATGTCT  
CTGTTGCTCC ACCGACCCCC CTGGTCGTAA G

16\_138 147

GGATCTCCAT GTCCCACTCC GCCAGCTTCT GGGGCGGCAT GGGGTCTGGG  
GGCCTGTCCG C

G/A

GGGATGGCTG GGGGTCTTGC AAGAATGGGA GGCATCCAGA ACAAGAAGGA  
GACCATGCAA AGCCTGAAGT ACTGCCTGAC CTCCT

16\_139 131

Table III

CAGCCTGTTA AAGGAATTCG ATACCTCCCT CCCTCCAAAC CCAAATCCAC ACCC  
 A/G  
 CTTCTCAGCT TACCAGGGGC ACAAATCCCA CTGGCATCCT AGAGGAGAGC  
 CTCAAATCGT AGGAGGCTGG CTGGGT

16\_140 133  
 GAGACCACCT CCTGTCAGCT CAGGCTGAAG CTGAGAAGGG GAACCTCTGG  
 ACAGAGGGAG CTC  
 G/A  
 GACATCCTTG ACTACAAACA TCCTGACCTG ATTCAGCAAG TGGTCTGGTT  
 TCCCCTGGTG GCCCCAGAA

16\_141 124  
 GCTGACACTG CTCTTCCCGG CAGCAGGGCT GGGAGTCCCA GAGCAGAGAG  
 GCCTCCTCTG AGTCCCTGCC GTGTCC  
 A/G  
 CAAGCTCATG TCTAAACAGG AGCTATGCCA AGCCCCTGGT TTCCGCA

16\_142 99  
 GGGTGGGCAG GGTCCCTGGGT ACGTCATGCC TAGGGGCAGC CTCAGCAGCC  
 CA  
 C/T  
 CCCCCTCTG ACCTCTGAGC CCTGACCACA GGACAGCAGC GGCTTC

16\_143 115  
 CATCACTCAG GGACAAGTCC CTCTGGCATC CCTTGTGGCA CCATCCATTC  
 CTAGAGAAGC CAGGAA  
 C/T  
 GTGTGCACGT GAATGAGGGG GCAAAGCCAA GCAGAGGGCT CTCTTCTG

16\_145 136  
 AGAGCCAGCT GCTGCCAGAA GCTATTACTG TTATTACCGG CCGGCAGCAC  
 AGGCTACAGC CACAATC  
 A/G  
 TAAGAGGGAA ATGGACTGAA TCCCCACACC CCAATCCCTC ACTCACTCCG  
 ACCCGAGGCT GTCTACCC

16\_146 137  
 GGTGTGGCGCC AAGGTTTAGG AGCCAGCACA GAAGCCTCTG AGAGCCATAA  
 GGGT  
 A/G  
 GAAAAGGTTA CCCGGTACTA AACCAGCCAG CTCGGGGTG ATCTCATCCA  
 CTTCCCAAGA TAAGCCCCCT CCCCCACCCT CT

16\_147 123  
 GAAAAGGTAG CAATTCCTC CGGGCTGAGG ATACTCCCAG TAAAAGGAAT GGTG  
 C/T  
 GATTGTGGGC CCTGCTGTGT CAGGAAGTAG AATCAGATGG AAGAAGTTTG  
 TTTGGGATGA CATGAAT

16\_148 148  
 AATTTTGGTT TGGATCTGGG TAACCTAAGA GGAAGAGAAG ACTAATCCAA  
 CTGCCACACT CTTAGGCCAA GCCTGAATTG TCAGGAT  
 G/A  
 CCAGAGACAT AATCAGAGGG TATCGATAAC TTGAGTTACA CCAACACCAA  
 TGGGTCAGAG

Table III

16\_149      145  
 TCAGAGACAA AGCTGAGGAA TAACAAGGAT GACTTTTCTA ACAATAGATC  
 TGATGAAGTA CTGGACCAGC CAAGGGAATA TCGGACA  
 G/A  
 CTCCTTCCTA GACATTTGCT GAACAACCTGA CTTTAGATGA AGTCCTACTC  
 ATAGGTG

16\_150      142  
 AGCCAGACTG AACAACTGT AATTCGTCAA ACATATCAGG TGAGG  
 C/T  
 GTGAATGTTT TATTCGGCTC CAGGTTCTGT GCATGCTGTT CCCTCCTGGC  
 AGGTTCTCTG CACCCCTCCC GCAAATACAG GTAATCTCCT CAGGTC

16\_151      133  
 TTCCCCGACT CCCTTGTATC TTCTCCCTGC CTTCCAACAG AGAGGGCAGC  
 AGCCTCTCCC AACTGGCT  
 A/G  
 ATTCTACGCC TTGCCTTTGA GGGTTACTTC ATTCACTAAA ACCGGTTCCT  
 GCTGCCCTG TTCA

16\_152      108  
 TGGGGTACCC CTGGGGGAGA AATGGGGAGG CCAGACCCAG CGGTAAGCCA  
 GGGGGA  
 C/T  
 GTGTGGAGTC AGCACCCAGT GCTGTGGGAT AGAGGGATCG AGTCTGGCCT  
 G

16\_153      146  
 CGCGCACTCT ACGCCTTCAC CGGCCTGACC CTCACGCCAC AGCTCGAGGC  
 CTGGATCCAC AACATACCCC ACGGGTCGGG GATCGGCAAG CCAATCGA  
 G/A  
 GCCTTCCATA CTTCGTCTAG GAATGCGCGC AACGTCTCCC AGGCCTG

16\_155      145  
 TCTCCAACCC TCAGTGCTGG GGGAAATGGT GCTTCATGTG TGCTGGG  
 A/G  
 TTGTCAGCAC TGGCTCAAAG ACTGAGTCCA CTAAGGATAC AGAGCAAAGG  
 TACTCAGGAC CAGCACTAAT GAGAGATGAG AAAGCCAAGG CTGGCAG

16\_156      117  
 CAGGACTCAT TAGCAGGAGC TCATAAAATG AAAGTGGCAG TGAGCTCATA  
 TGGAAGA  
 A/G  
 GCATCAGGG CAACTCGGCT TGGCTCACCA GCCCCTGAGC TGCCCCCGAG  
 TGACCGCTCC AGCCTTCTT

16\_157      124  
 AGAGGTTTCTG GGTCCCTATG GGTATCACAG GAGGAGCATA TTCAGAG  
 A/G  
 GGTAAAGA GGACATGATC TTGAGGTGGA ATAACATGGG TGCCAAAAAT  
 TGAGGAGTGG GGTGACTAC AGGGAG

16\_158      149  
 CTAACTGTC TTCCCCTTGG CTTCAACCCCA GACTCCTCTT CCACTCCTGA  
 TTCAGGAGGA AGCCTGTTCC  
 A/G

Table III

CCTGCATTCC CCATCGCATG GTCCAGCCAG CCTGTACCCT TCTCTGCCTC  
 ATCCATCACC CGTTCTGCCA GCATGGGT

16\_159 141  
 TGGCTCCTAG AAATACTTCA GATGCCATGA GATCCACCAC CTTGAAATGT  
 CAAAGCAGCA AAATTCAAAC CCAGGGGCCC TGGGTGCCA  
 A/G  
 TGAGACAGCT GTTATCTTTT TTA CTCACCA GACGAGGTCA CAGATAGAAT  
 G

16\_160 142  
 CTCGTCATTT GTGTGCACTA AATTTTGAGA ATCACTAGAT AATTTTCAGC  
 TCTGCAGGCA GTTCCTGCTT C  
 C/T  
 ATCACATGGG GCCTAGCCAA CAACTTAGAA TTGAGACAAA CAAGTATCTG  
 TACCTTGGGT TGCCAGGAG

16\_161 116  
 AAGCCTTCAG GGGAGGCAGA ACTAGGAGGG CCCTGGAAGT CAGGGGGCCT  
 GGGATGGA  
 T/C  
 AGCCCTCTGT GGGCCCCCTCC ACTGGGATTC CCAGAGGCCT TGCCCCCTATT  
 AGTGCCGGGG ATGGCCC

16\_162 112  
 CAGAAGGAGC GGGCGGGACT GGCAGAGGGC CAGCATCCTG GGAGAGAAGG  
 GCTGGGCTCA AAGG  
 C/T  
 GAGAAGGCAC AGATGGCACC CGTGAGCCAC GCTGGCACCT TCGTGCT

16\_163 146  
 TGCTCCTCCT CCATAGAGGA GTTATTAAAG CCACAGAGTT AAAGTAAAT  
 GGCCCGAGAG CAAGACAATG AATATCAGAG AGGGTCACAG GA  
 C/T  
 ATCAAGTGGA CTTGTGACCT TGGGAGTGTA AGCACCTACA GTGGACAGAG  
 GGG

165 141  
 TGATAATGTC AACAGCTTTC GAGAGCCTCT GAGCAGTGAA TGAGATGATA C  
 A/G  
 GGTGAAAGCA GCTAGCGCCA TACCTGGCCC AGGACAGGCA GGAAAAATGT  
 CAGGCAGATC TGAAGCTGAA TCCGGTTACT GAGTCATCA

16\_166 125  
 CCAGCAGGGA TTAGAGCCAG GGGCAGGTGT CATGGAAATT CCTTCCACCA  
 C/T  
 GGCCTCCACT TACTTGACTG GCCGGCTTCC TCTCTTCTGT GGGTTTAGAA  
 GTCACCCGCT GGACACCGCT CCTT

16\_167 106  
 GCCCCCTCTG GGCCCTGCC TAACAGAGGG ACAGAGAGAG GGCTGTGTCC  
 AC  
 C/T  
 CTGCAGCTCT CTGGATTGG CCAAACCTGG CTGCTGTGTG GCCATTCTT  
 GGG

Table III

16\_168            130  
 GCTCACCACGAC CCTGTGAGTA CTGGCTGCGT CTCTGGGTGG CTCTCTTGTG  
 TCTGGTCTAG TGTCCCTC  
 A/G  
 GGTGTGGCTG ACCCTTTGGA GGAAGCAGTG CACAGGGACA TATTGACATG  
 GGTGTGGAAC AA

16\_169            127  
 GTGTGAGCTG GTCCAGGCCA ACGGGAAGTG GGCAGGAACG GCATGGGTCA  
 CTGGAAGGCC ACAG  
 C/T  
 GGGAGAGTAT CCAGGGGTGT TCCTGTGTCT GTTGCCCGTG CCGCTGGTG  
 ATGGGACATC AG

16\_170            122  
 ATGGTTTATG TCAAACCGGA GAATGGCCCA GCCCGGCCAG GGGCTCCAGG  
 ACAGTTCCCA GGTGTCGG  
 C/T  
 GGCTCCTACT TTCCTACTCA AGAGTAATTA GAGGGAACCC TTTTAAACC  
 ATT

16\_174            132  
 GGGGCCCTTTC TTAGGAGAAG TTGACTTCCT GGTTTTGAGT TGAATGTAAC  
 TCTCCTTGC TGG  
 C/T  
 TTCTCCGCTC CCACCATTCA TTTCATAAGG ACAAGGTCAT GCACATTGTA  
 ATTCTACGGG TCGGATCT

16\_175            144  
 TTGCCGCTCA GCACAGGGCG TGAGTCAGCC CCAGTGGCCT GAGGCGTGT  
 TCAGTTTCCT GCTGA  
 C/T  
 TCAAGGGTCG TGAGTTTAAA ATAGACTTTG CCTGATAACT TGGAAATGAG  
 GGAGATTTAG GCTGCACTTA AAATGAGT

16\_176            135  
 CCCTCTCCAG TGAGGGTGGG TCAGAGTAGA CCCCTGACTG GGCAGATGAG  
 GAGGCTGCTC AGAGGAGGCC TCCAGC  
 C/T  
 CTCCTGCCT CACCAGCCTT GCTTTCCTCC CCTCTTCCAC GGGAAAGCGGA  
 GCTCCTAA

16\_177            119  
 GTTTAATGAT GCATGAGGTC TTGACAAGAA CCTAAACACC AGCCTGTGGT TTG  
 C/T  
 TTTGGTTGTG CTGATGTCGT GCTGAGGTCA CAGCCCAGGA CCATGACCCC  
 AGAGGCCCTG ATAAA

16\_178            113  
 CAATCTAGAA AGCGGGGCAA TGGGTAATCA GTCTCACCGT CACTAGGC  
 C/T  
 GAATGGGAGA AATGCTCCTG TGGACATGGC CTCCCAGTGT GGGTGAGCAA  
 AAGGGCAGGC TGAG

16\_179            139  
 TGAAACATAC GGTGCAGGCA AACTCCAGTT TTCTTGCCCT GCAGGTGAGA CCACC  
 A/G

GAAGTGCAGT ACTTAGGGCT CCAGGAGCCC CTCAGTTGCC CACAGAAAGTA  
GCTGTTTAT TAACACACCC TCGATAACTT CCT

16\_180 148  
CCCATGAGAC ATGGAGGGCC TTTGAGAGGA AAAAGCCCAG ACCTGGCCCA  
GCTCTGGGAC TCCACACGTT AGGAGGGGCT GAGGC  
A/G  
AGGAGCGGCC ACCCTGCCAA GCTGAGCCTT ACAGGCAGGG GCCATGTAGC  
CTGCCGTCCA CCG

16\_181 125  
AAGGTAAGAT GACGGCAGAA CGTCACGGAG GAGCAGGGCA GGGCCC  
C/T  
GTTAACAGGC TGAGCCGGGC GCAGGTGAGC AGACAGCACT CGGCACAGGG  
CCTGTCTAGA GCCTGCAGTC ACACCTCC

16\_182 146  
TTTCTTTGAG GGATGTCTCA ACGCACCAGG ACAGCACGAG ACGCCCAACC  
CGAAG  
C/T  
GGCTGCTGCC ACCTGAGTGC GCCCTTCCAA CCTGAGGTCT AAAATGGGGA  
AGAAAGCTGC ATCCCCATCC CGCTCCCGGG CAGAGCCAAT

20\_001 110  
TAGACCT TACTATGTGC CGTCCTAGTC GCGCTTCGTA TGTGTTAAGC  
CCTTT  
A/G  
TCCCTCACTC CAATCTGTGA CATAGGCACT CAGTACCCCG TTGCCCAAAT  
GAGGAAA

20\_003 144  
AG CACTTTCGGA AGCCGAAGCG GGTGGATCAC TTGTCAAGAG  
TTTGAGACCA GCCTGGCCA  
A/G  
CGCTGGTCTC CATAATACTC AGCCTATGAA GAACCAGGAG AGGGACCTGC  
ACACTAGAAG ATAAATTGCT TGTTGTAAC GT

20\_005 146  
GATTGTCTCT CTGGACACGG CTTATGTTGA CAACCTGGAT CACATTAGAG  
GATCACACTG AGACCTTTAT GTCGGCCTCA GTT  
C/T

CTCCATCTGT AAAGTAGAGG TTGGGCTTAG ATTATAGATG ATAAAGACAC  
CAACTTTCCT GG

20\_007 112  
G AATACATGCT ATCTTGCTTG TAGAAGCCCA GATTCTCCT TCTTACGACT  
CCCA  
C/T  
ACCCACTTAG GAGATTCTAT TATGTCTTAA AAGAAGTTAC ATCTCCATTA  
GTGTCA

20\_008 145  
CAGGT GGATGGAGGC TGTTCTCATC TGGGGCTGTC TCTTGATTAA  
GGCTGTCACC TGTTTGTATA GGGACCATGT TTCCCA  
C/T  
GCACTTTGAG TGCAGTTTAG GAGGTATCCT TTGGATGCTG AAGTGTGGG  
ATTTTGAGGA CA

Table III



20\_010           132  
 ACAA GACTGCAACT TACATTCTGT AATGAAAGTT TCCATTCATT  
 TGTTCACTCA ACAGTTATTG TATGCTAGGC A  
 C/T  
 TGTGACTGGA GTGAGGAATG CAGAGATGCT CAGGAAACGG TTTCTGCTCT  
 CACCCT

20\_011           126  
 GCA AGTTGGGCAT GTATCCTCGT GACCACTACA GATGTGCTAT CT  
 C/T  
 AATCGTGTAT GTTGAAGACT AAATGTTTTT AGTGTAATAG AACTTGACCT  
 CAAATAGAAG ATTGCTTTTA

20\_012           128  
 TGTT TTCCATGAAT CATTTTTATG TTTTCAAAG GTTTACTCT  
 TTTCTCTCTG GTAGTAATCA CACCAGGAC  
 C/T  
 CCTTTCATCT TGTACTTTGT TCTCCTCCAG TGGCAAGGTT TTGTGGTCCA  
 GACC

20\_013           145  
 CTGTGGGA AGGGGCAGCT AAGGCAACTT GGAAGGGATG AGTATAAGGA  
 AAGATATGTG GATGCTAAAG AATTGGGATG AAGAAGAAAT CTATG  
 A/G  
 ACCAGTTGCC CAAGTCTTTG ATAAATGAAA CGAGTGACCA AGATCTGGAT  
 A

20\_014           110  
 TGCACACAG CTATACCTTC CTGGTTCCTG AGGATTGAGT GTCCCCCTGCG  
 T/C  
 GCTTAAAGCT GGAGCCAGAC GTATGCAGCT TTTTCCCGCT GTCCCCAGGC  
 ACCGAGTACT

20\_015           138  
 TCAC TGCAGTGTCT GCATGACATA TGGATAGTAC AGAGACCTTC  
 AACTATATT ATGATACAGA CCAGGAAAAT TAACATAGCC  
 C/T  
 TAGGGCAAAA CACTGAGTAA ATATTTATGT GAATGAGGAC TGTTTCTGAT  
 CTT

20\_017           140  
 CCCT ACCTGTGGTT  
 CCTTCTGCAC CCCTGCCCTT CAGATCTGTG ATGGGCAGGA CCAAAGAGCA  
 GGCCGAAGAG CTGGAACCAC GAGCACAAGG  
 A/G  
 CCATCTCGGC CCACTGCCCT GTGATAAAAT GTGGCCCACT GAACA

20\_019           146  
 AAATA AGGTAAAGCC CTTGACCTCG AAGAGTTTTT AGTAGTGGTT  
 GGAGGAGTGA GGGTAGAGGG TGATA  
 A/G  
 CTACATATAA ATGCATTATA CTATGAAAGG TATGTGGTGA AGTTATTGTA  
 TTAGTCCATT TTCACGCTGC TGATA

20\_021           142  
 GAAAT GAAACAGCTA GAGATGTTAT GAAGGTATAA GATAATGAGG

Table III

CATAAATCGT ACTCAAGCCC TAAGGA  
 C/T  
 ACTCAGCATG TAGGATCCAT TAACAAAGAA GGGTTACTTA CTAAAGAAGA  
 TGTTTTTTGG AGGGGTGCCT

20\_023 126

GAG  
 ATCCACTGCC ATAGAAAACG TGAATGATGC TCTTCTTTTA AAGGTCAC  
 C/T  
 AAGGACCTCA CATTCTTCAA TCCAATATGT ATTTTTCAGT TGCCATGGAC  
 TTTACCATTA GACACCACTT ACCA

20\_025 148

GGGGG TTAGGAAATG TCAATAAACG TGTCATAGCA ATTTTAGATT  
 TTAGCAGTGA GAAAGTATGA TTTTAGTCAA ATCTTGAAGC AGGTGA  
 A/G  
 GAAGTACTTG CCAGGTTTCA GTGGGAGCCA ATCCCAGGCA GAGGCTACAG  
 CAGGTG

20\_026 138

CAGAGGAT TGGAACAACA GATATGGAGA GAGTACAGAG  
 CAGACAATGC TGTGCAGCCT TGTTTGAGGG CTGCTACAG  
 A/G  
 ATGCTATTCC ATTTGCTCTT CGGATTCAAA GTTCGGGTAG AGAGTCCAGC  
 TAGCCAGGCT

20\_028 139

TAAAGCCA TTCTGTTGCC TGCTTCTCTT TCTGTGGCTT AAACAGAG  
 C/T  
 TTGCAGTGGC CTGAAAAGTC ATCAGTCATG AGAAACAAGC TTTTCTAAAC  
 ACTAGGCCAG ACAGAACAGA TTAGGAAATC TCCAAACTGG AT

20\_029 118

AGG GAGGAGGGTA TGGGGAAAAA TTGATGGGGA AGCCCCCAG ACTTTTGCCT  
 TGTGCCCAGG ACAATGACTT  
 C/T  
 TCAGCCAAGC ACTCAAACAG TATGAAGCCA ATTTGCTGGG TTCA

20\_030 136

TTT TGAATCCCAG ATAAAAAAGG AAAATACATC TGGCACTTCT  
 CCCTCTTTGC CATCCTGCCT TACTCTCACT TTGAATG  
 C/T  
 AGATGTGACA TCTAAAATTT CAGGAGCCAT ATCACATCCA TGAGGCAAAG  
 GTATA

20\_031 137

AGAGGGG TTTAGAAAAG GTTGCAATGT ACAGAGGGGT TTTTAATTTG  
 TATTAATATT TCTCAGTTTA CTTCCCTC  
 C/T  
 ATTTAGATTT AAGATTTACT CATTAATTCA ATAAACATTT ATTGAGTGTC  
 TGCTATGTAC CA

20\_032 146

CACCTACGG TTGCTGCAAT CTCCTGCAGC ATTTGTACTG GTTGGTATCA  
 TTTCTCACT ATTGATTCA  
 A/G

TTACCTTATC TAGGTCCTTA GGACAAGAAG TGAGAAATAT GATACCCAAC  
TCTAAAGAAA GAGGTTTGA AGGGAA

20\_033 135  
CATT CACACATTTG GGTGGCTTG GTGGCTCCAC ATTCATTACA GGCTAG  
C/T  
TCCTGGGGAA CCTGGGAAAT GTAGTTTTAG CTTTTGTCT TCTATAGTAT  
AGCAATCAAA GTAAGCTAGA AGGGTGTGG AATA

20\_034 144  
AGGC CTTGTTCTAA GTGCTAGACT GCAGTGGGGA GAAGTCACAA AATC  
A/G  
CTCCCCTTTT ATGTCTGTAT TCTAATATGG CAGAGGGGCA AGAGAGAGTG  
AACATTGAAT TCAAGAATTA ATCCTACCTG CTACCCACCT CGACT

20\_035 148  
GGAT ATTCAAAATG CCTTTTGTAT  
GCTCATTACA AGTTTCCAAC TGTGTTCCAG CTAGAAGGTG TGAGGTAC  
A/G  
TGATAGCTGT ACTACTAAGG ATTTGCCATG AAGTACAGTG ATCTATAAAA  
GAATATTCCA GACAAGCAGT TCCTT

20\_036 147  
A CAAAGCCACA  
GGTGCAAGGG ATGCAGAGAG GGACAGGGCA CAGGAAAAT GCTGGGAACT  
A/G  
GTATGCGAGG AGGAGGTGCT TACAGGACTG CACAGAATCT CAGGGCCCAG  
TGCCAAAAAA ACCCACAAGA CCCCTTGTTT CAAAT

20\_037 125  
TTGGCCG CTGATCCAAC AAACCAACTG TAAAGGAAT TTCTGAAACA  
ATTCAAAAGG TGTGACTACA GGTGACT  
A/G  
CTAGATAATT CCAAACATGT TCATCTTGTT AGAGGACTGA TAATGAACA

20\_038 113  
G AGACTGTTAC AGCCACTGTA GGAGTTTCAC CTCATTCTAT CCTTCAACA  
ACCCAAT  
A/G  
CGATAGATGC TATTATCCTC TTTAGGATAA AATCGAGGAA ACTGAGGTAC  
AGTG

20\_039 135  
GGTGGATT TTCTTCAAAT  
TCTAGAAAGT GAATTTCTAG TAAGTTCCCC TGGCACAGCA CCA  
C/T  
GGTAACTTCT CTGCAAAAGA CTCACCAAGC CATGGCCATG CCCTCCCAAC  
TAGGTCTGGA TCAGCCCTGG GGA

20\_040 125  
GAA TCCTAAACTT CCTCATCAGC  
GGTGGATTCA GTTATGGGCT CCAATGTTTC ACCCCTCCGT GAA  
C/T  
CCATGCCCTT ACTCTTGCAA CTTTGCAGTC CCTCCCGCTA AAGACAGAAT  
GAACTCCT

20\_041 135

Table III

CTTAG ACCAGATATG CCTCAATTTT CTTTTCTAAG ATGGTGGCTG  
 TGGCCTCATA CACTTCACAG GGCTGTATAA ACTAAGCAC  
 C/T  
 AGTACGTGTG AAGTGCTAAA ACGGGTGTCC AGCACATAGT CACTGCTCAA

20\_043 147  
 CAGAT  
 GGGGACAAAG AGTAAACTCT ACATCTCTAA AATCTAACTC AACATCTTTT  
 TCTCAAACCT GACCCTTTCT CCAGATGTTT  
 C/T  
 TGTTTCTGCT TCATTTTCTGCT ATTCTTCCTT CCAGTCACGT GTGCTCAAAG  
 TGCCAAAGTT A

20\_044 92  
 GTGAGTGTG GACAGTCATT TTGCTAATTC TTCTCATTGG TGGTTCC  
 A/G  
 CTAGATGGAT GATTTCCCTG AATTAGCCAT CATAACTGCC ATCTG

20\_045 134  
 G CCATGCTTCC ACATGTGTGT ATGCTGTGTT TTCTCCTACT  
 TTCTGTTGTC ATCTTTGTGA AGACAGTGCC TACAACCCTC  
 C/T  
 CCTTCAAAG ACCTACATCT TTTATCTGTG TCTGTTGGTA TATTTCCATC  
 AA

20\_046 114  
 GAGAGA GAGAGGGTGC GCATCCGAGT GAGCCAGTGT TAGCCAAGAA  
 GCAGGGAGCA GGGCTCGAAA GTCGC  
 C/T  
 GAGCGCCGAG TGCGAGGAGC TGTGATTGT TTTCTGGTTG AA

20\_047 148  
 CT GAGGAAGGCC TGACCTGAAA CGATTTAACT TCTATGTGCA  
 CACTCTGAAT TAGTTTCTGG AACACCTGAA AATGCTCCAA AGGTCCCTCT  
 GGAG  
 A/G  
 CCTCCATGAA ATGTTGGTTA GTTAATGGAG TGGACCTAAT ATTAGCCAGT  
 C

20\_048 146  
 TAGCAAGAG CTCCAGGCTC TCGGTCTTCT GCAGCAGGGC TGCCTCCTCC  
 GTCAAGTGCA GCATCTTTTA GGAAAGGAGT GTTCCTAGCC TGGCAGTG  
 C/T  
 AGTTAGGTAG AAATGAATGA GATGTCAGAA ACAATATTGA CTCTGAAT

20\_049 147  
 GAAGCCTTT TGGGAACTCG GAAGCACTTA TCCTCAGACA TGTGGCTCAT  
 TCTTGTTTCC TCCAGGAGCC AATAGGTGGT AGCAACGGGC CAGCAAAGAA  
 A/G  
 CACCTGCTAA GGTGGGTGGT TCAGCCTAGC TGTCAAGGCG ATAGAAG

20\_050 128  
 CCA AAATTAGTGG GAGCTGAGTA ATGACTGTGC CTTTAACTAN  
 GTCATGAAAT CACTGCCCTT TCTGGCTCCT TG  
 A/G  
 CACTAAGTCT GAGAATTAGT TCCATTTACT AGGCAATGAC ACTGTTGTTT  
 TC

Table III

20\_051            96  
 GGCCCCCTGG TCCTCCATCT AAATGTTGGA GTCTGACTGC CTGCAGC  
 A/G  
 CACATTGGGG TCACATTCCT ATGCCTTAGA GAGAGGAGAA GCTGGGTG

20\_052            119  
           AGGG AAGCTGCACC CAGGGCTTCA CCCACAGGCA CCATCGCTTA  
 CTCTGCCTGG CTCG  
 C/T  
 GGGTCGGTGA AGGGAGTGGC TGCCCTTCTG CTCAGCTCGG TCTTTGTCCC  
 ATTATTTTCT

20\_053            146  
 GAGAAAGCC ATCTAAACAG CTATTTCAAC ACAGCGTGGT GCAGGTCATC  
 ACACGACACT AAAAG  
 A/G  
 TGCAGACGCT AGTGCCGTGG CTCCAACCTT GGGGGTCTCC TGAGGCACAT  
 CTGGGGCTTT AACACCAATG CTGCACCCAT G

20\_054            127  
 TTGCAGGAT AAGATTTTGG GTTTCGTTTT CAGCAATCTC AGCCTTGCGG  
 T/C  
 TACATGAGAT AAACATCAG AACAGACATA GATGCTTTCA AGTATTTTCA  
 GCAGAACTTG ACCTGAAATT TTGAATC

20\_055            93  
 GAAG GGAGTCAGCG GAACTGGCTG GGGCCTGGCT CCTGCTTGGC ATTC  
 A/G  
 TGCCACGTGT GGCTTCCTCA GGTGGCCAGA CCACTCTGTC TGAG

20\_056            136  
 TTGG TCATGAAGAC ATTTAATGGA TTCTCTGAAG TGGTGGCAAG  
 GTGGCAAG  
 A/G  
 AGAGTCCAAC CTGAAGCTGC AGAGCCTGGG ATTGCGCTGC ATGGAGAAGA  
 AAGGGTGTGC GTGATTCCAC GTCCTTTTC ATC

20\_057            127  
           GCAAA GACCCCTCTG CACCGGCGAG CCAGCACCCC ACTGCCCCTG  
 TCCCCACGGG GCC  
 A/G  
 CCAGCCTGGC CGCCTGAGCA CAGTGCCTTC CACTCAATCC CAGCATCCCC  
 GGCTGGGCCA ATCAGCCT

20\_059            147  
 C TCTCTCTCTC ATGCATGCTC ACTTTCTTCA ATGAGTTGTT GCACATTTAT TGAGCATCTA  
 CTATGTGCTG GCACTGTGCT AGGGACATAG ATAAC  
 C/T  
 AAGGCAGGGC TCCTTTACAC CAGGCCTTGT TAGCTAGGAA AAGGGACCAG

20\_060            110  
           TGATGCCTT CATGCTGCAT CTTTTGGAAG GGAGGAGCAT TGTGTCCTCA  
 CAGAGCAGAA AAT  
 A/G  
 GAAGGGCCAC AGGACAACT CCCTCTATCA AGCCTTTTCA TAAGGGC

20\_061 132  
 CATCG CATTGCCGGT GCACTCACAC ATACCCACAG TTA CT CAGAC  
 TGGGACCACA CAGACATGTC AATCGACCTC ACATGC  
 A/G  
 CAGCCTTGGG AAGTGAGAGG AA ACTGGAGC ATCCAGAGAA TATCCATGCA

20\_062 125  
 ACACCATT TCCCACACCA GCTTACACCC CTGGCACGTG CACCCAGAGC  
 CCCCAGTTCT TCATCAGGCC AGTCATCGTG  
 A/G  
 TCATTGTTAT CTACTAACAT CACCTGAATT TCTCAGGAGC TTA CTG

20\_063 143  
 CACTGC ACCCAGCCGG TTATGCGATT TTTATCAGAC CTTAGATATC  
 TCTTATATAG ACAGGCAGAT TATGTAGTTA CAGACAGTAC CTCAGAAGTT  
 C/T  
 GATGTCTGTG ATCAGTTTGT CTTTCGAAAT CTTGCTCAGC AATGAG

20\_064 125  
 TGGAAG GCTCTTAGGA CTGCTTGAGT GTCTTCACAA CATGGTAGCT  
 G/A  
 GCTTCCTTGA GAACAAGTGA TCCAAGACAG CCAGCAGCAT CTTTGGATTG  
 ATTTTCTTGT CAGCAGTGGG GTGTAGTG

20\_065 145  
 CAA GAACACAGCT TCAAAAAGGT CGCACATAGA GTGGTCAAGG  
 AGGAAGGGGA CACC  
 C/T  
 GCCTACCCAG CCAGATCAGC CGAATCAACC CTGGTGATCA ATGGGGTGAC  
 AGATGTCGCA GCTAGATCGT CCTCACATCC AAAATAA

20\_066 130  
 ACATTC CCAATGACCA TATAATAGAG AAGGAGAAAC AGTTTCTACA  
 TTCCCATATG GTATCTTAAA GATTTAAC  
 A/G  
 TTTCAAAGAT CAAGAAAGTT TACTTTCTTT CAGATTAAAT AATGAGAAAG  
 GCAGC

20\_067 129  
 AGGCTG CAGATGAAGA GATGCATAGG GTGAGGTATG GGAAGGGGTG  
 CAGAGCTTCT GCGTCCTCCC TGGGCCT  
 A/G  
 CCACCTTCTA GGAACCCAG CATGTCTGGC TATCAGGAAG CTCTC

20\_068 142  
 CAGACAC CTCAGGGCTG CATTAAATTGG AGGGACGGCT CTTGTTATAG A  
 C/T  
 GAGGAAGTCT GAGATGTCGT GCCATACATT GCTGTCCTCA TAGAGGTAGG  
 TCATGGAGGA CTGCAGCGAG GGCTGCAGGG TGGATCGGTG ATAC

20\_069 105  
 GCCGCGTG TCATGAAATT CGAACAAGAA GTACTGAATT GAAGTGGGGA  
 TGAGAGGT  
 C/T  
 AGATGTGAAG GGCTCCTGCC AGCTTACCCA GGTCTCTTGC TCAGAAGA

20\_070 116

Table III

CAGAAGCAG GAGCTCAGGG CAGATAGAGG CCTGGAGTGG GCTCTGCATA TGTTC  
 A/G  
 GAGGTGAGGA TGCAACAGGA GAGTGTCTG CTGTCAGGAT TAGAACCCCA  
 AGAAAGGGGT

20\_071 103  
 TTGGGATCTG GTTGGTGGTC TCAGGGATAA AGAGGTCAGG AGTCATCCAT T  
 C/T  
 CTGATTGCTT CCTGTCTCAG CCTCACATCC AGCCCAACAG AAAGCCCTGT  
 T

20\_072 128  
 GGGGA AAGAAGGCCA GGACACGCAG CCTGGCATCA CCGTGCCACA  
 T/C  
 GATGTCCCCA CTCCAGACAA CACAGAGGCT GCCTGGCCCT GGAGACTCAC  
 CACGTCTGC TCCTCTGGTT GGAATAATG AG

20\_073 123  
 CG AGGTCCGTGC GTTGCCGCTC GGCCGCCATG TAAAAGTGGG TCAGCT  
 C/T  
 AGCCTGGAAG GCCCGCTGGG TAGAGGCAA GGCTGCCAGC TCTGGGAAC  
 CTGCACGTT TGCCTCCCCA GCCCCT

20\_074 120  
 A CACCCTGCTG CAGACTGGCT TCCCCTGCCG TGGGTGAGGC AGGACAGGGG  
 CACACCAG  
 C/T  
 GGGAGGGCTG AGAACTCTTT ATGACAACCT TCCATCTAGA GAGAACTCTT  
 TTAATTGCCA

20\_075 108  
 G AGATCAGATT AATGCCATGA TTACTGCTCT GTGCACCTTG TATGTCCTCA AAGAGATGA  
 C/T  
 CCCACATTC TGTGAATGTC CAATCTGATG TGTGAGCCGT CTTTGAC

20\_076 116  
 GTTCCACTG CAGAGACGAA TCGGTTCATT CACAATGATG AACTCATCCT  
 CTACTGACGA ACA  
 C/T  
 CTGAACTCTT TCCTGTGTTT TGCTATTATA ATTAGTGTTG CAACGCATGG  
 CCT

20\_077 131  
 TGGGAGGAA ATGTTTATAA AGCATATATT TGATGAAAGA TTTGTATTCA  
 GATTACATAA AGAACTCTCA G  
 G/A  
 ACTCAATAAT AGCCTTTCCT TTTGGTGGTG CACAGCAGCA ATATGGTGGT  
 GAAAATTCT

20\_078 115  
 GGACCTTGGG TGCAGATCAA AACTAAGCT CCATGTCCAG CCAGGTAGGC  
 CCCACACTC  
 C/T  
 ATTCTTAGAG CAGAAGAACT AATTCCAGCT CTACCTTCCA TGGCTGGAGT  
 CTGCT

20\_079 109

Table III

GGCCATGGCA TGTGTTTACA AAGTTATTTT GGAGATAAAG TGAGACAATG A  
A/G  
CAGAAAAGGC CGAATGCAGT GCTCACCAC TATTTTTTTT TCTCCAAACA  
TAAGCAT

20\_080 137  
GGATCTAGA ACAGCCCCTA GTCCCACCGC AGAGTGGACT TGGT  
C/T  
TCCTGGCCAA TTGCAGGCAA TGAAACTCTT CCTTCTTCAT CCTTTCTACA  
TGTGGAATCA AACCTAGAAA TACCCTTAGG AAGGAGTGA TGA

20\_081 111  
TAAC CCTAAACTGA ATCCTCTCTA GAGTACAGTA TATCCCAGGG  
CTCACTTGGG GTTCTGTTT  
C/T  
CATCTCTCCA GAGCATTATC TCAAACCTAC CCAGACTCGC CCACTAT

20\_082 101  
CATTTG GTAGATGGGT CTGTAGCTGC TTTGGAGAGG GCACCC  
A/G  
CAAGCCAAAT AGAGAAGGGA TAGGGTGCTT GCCAGGCTGT CCCCTAGAAG  
GAAAAGGT

20\_083 131  
TCCCAGGCTT GTAAATACGT GGGCCCCTGA ATTATCTGTT GTGAGGCTGT  
TATCTAGAAG CAGGGGTTTG GGGTTTGAAG CTAGG  
A/G

TCGAGAACCA TCAGAATACA AAGTACTGGA GAAAGAACAT TCCAG

20\_084 133  
CATCC TTCAGTGA CTGATAGT AGAGGGAGAG TGACCAACTG  
GCTTGCCACT TGCTCAGTCT GCCCAGGACT GA  
C/T  
GGGTTGCCCC GTACGTGGGA CTTTCAGTGC TAAAACCACT AATGTTCTGG  
GAAAA

20\_085 143  
TGG TCTCATGTCT CCGAATAAG TACTCAATAG CCACAGCTGA  
GGTGCCCTCAT G  
C/T  
ATCATGGGCA GCCACAGCCC CTGCCCCAGT CCCCTTGTCT GATGAACACA  
CATCATGATG CCACTCTATA AAGAGGACCG TTGCCAGA

20\_087 127  
TGGCCCTGAG AGTTGGAAC GAAGCCCATG TATAAAGACT GG  
A/G  
GGGCCGGGTG TGGTGGCTCA CACCTGTAAT CCCAGCACTT TGAGATGCTG  
AGGTGGGAAG ATAGCTTGAG CCA

20\_088 137  
T CTTGGCCTTG CTGAGATTC TAACTGGAAC ATGGAGACGA  
TGTGTATATA GGGAGGGA  
A/G  
GAGAAAAGCA TGAGTGGCTC TCTCACCAC TGATTGCTAT ATTTGATCCT  
CACTTAGTCT TGGGAGATGG AGCTCCT

Table III



20\_089      141  
 TGGT AGCCAGTGCA TGGTGAGCCT GTTTCACCAC TTTATTAGTC  
 TGTTTTTCATA CTGCTGATAA AGACA  
 C/T  
 AGCCAAGACT GGGCAATTTA CAAAGGAAAG AGATTTAATT GGAATAACAG  
 TTCCACGTGG CTGGAGAAAC C

20\_090      149  
 CCACTGTT CCCATATTCT CGTTATATTC CACAATGACA CATGGCCTCT  
 TAGTTTTATT TCCATTTCTG TGGTCTACCT CAATAACAGT AT  
 C/T  
 GTTGTGGAAT GTTGAAAACA TTGTCACCTC CTTGTCAGAC CATTTTGGTG  
 CCATAAAT

20\_091      118  
 G AGATCAGACC TAACCAACTC TATCTTGCCT CTACCCTTTA AGCTGTCCTT  
 GTTCATTCCCT GGGTGTA  
 A/G  
 GCAGAATAA CCTTAGGAAG GAATTTAGTT TATGGTTTGA CTGAAACAA

20\_092      134  
 GTC TGGTACAGTT TTCCAGAGGT TACATGATGT GTGATGATAT  
 CATCACTCTG ATAGCTAATG GAAAGTATGA  
 T/C  
 TGTATATTCT GTAATGTTCC AGGAGTTTCT GAGGTTTAGG TTTAGGTTAT  
 AAAAGGGGGC

20\_093      138  
 TCCACA AAAAATGGGA AGACTCCCCA TTAGGGAGCC TGATGAGGGG  
 TCTGTGAGCT GGTGCTGAGC CTGGAATGGG G  
 A/G  
 ATGCCATGGG TTGAGTTGTG TCCCCCTAAA ATTCATATGT TGAATTCCTG  
 AAGTAGTTGT

20\_094      133  
 AGTGCTG CAGTGAGCAG GCTTATCCAG CCATCTTTGC ACACATGAAT  
 GTTTCTGAGG ACATCTTTCT AC  
 A/G  
 GGTGATATTG CTGGGTTGTA GGTGACAAGC ACTTTGAAAC TCGACTCCTC  
 AGCCAAACTA CCC

20\_096      131  
 C GAAACTAAAC TTCACATGGA GCTCCCAAAG ATTTTCATAA  
 TCTGACTATT AATTTTCATT TC  
 A/G  
 ACCACCATCT TTCTAATTCT ATGTGTGTAT CTTATTTATA TGTCAGTTGC  
 TTGATAGTCT AGACCCT

20\_097      149  
 ATCTCCAT CCTGAGCATA ATTAATAATA CCTGAATCAG ATGTTTGATG  
 TGAAGACTGT ATTACTTTAT GAATGATGTT TCCCAAACAG TGGCA  
 C/T  
 ATAGAAGGCA TCTTTATGTG TATTTTAGGA GCATTAGCTT ACAAAGCGGG  
 GAGCC

20\_098      127  
 TGATGA GGAATACAT TCATTCAACA AATATCTATT GAGTGCCTCT

Table III

TTCACACCAG CTACCGGGCT AGGTAGCTGA ATG

C/T

TTGTCTGAAT GTTTGTGGTC TGAATGTTTG TGTTCTGCA AACTCA

20\_099 125

CCAG GGCCTGGACC CCGTTACCCT ACAGACCTCA CTACCCAGCC  
CTCCCTCTCA CTCCTGCTC CAGCCCCATC AGCTTC

C/T

TTCTGCTCTT CCAATGCGCC AGACACGGTC CCACTTCAGG GCCTC

20\_101 120

CTGG ATGGAGTTGA GTCAAACCTGC CTCTGGCCGC CTCCAGCTTC  
CTGCTGGGCT TTGCT

A/G

TTAGGGGCAC CAAAGAAGAT CAGAGGGTCG GAGAGAAAGG GTTTGCAAAT  
TTGCAAATAT

20\_102 106

TCTGAGCAAC TGGACTATCT TTCCAGAGTC CAGGGATTCC AGGTAA

C/T

TGTCTGGCCT GAGCTGTGAT GGCTGTGCCT CAGGACAGTC ATCTTTTGGC  
TTCTCTCAG

20\_103 126

GC CGTTGTTTAT CGCCCTCCCG TGGATTAATC CCCTGTCAGT  
TAGGCCAGAG AAGCTCTGGA GAAGGCCTGC

A/G

TAGCATCCCA TGTGTCAAGG CCCCCTTTGA TACACTTTAT CTGCCCTTAT  
CCC

20\_104 148

CACATG GCACAGAAGT GCTTATAGTT AGGAAACAAA GGCTGGAATT  
TCTTTATGCT CTGACA

A/G

CCAGGAGGTG CTGCCCAAGA CTCTGAAATG ATTCCTGAGC CAGCCCCCAG  
GCCCTGCAG TAGAGTTTGA GTCTAAACCA AAGTG

20\_105 120

CTTGCCCTG CCCCCACCAC CTTATGTCTG TGCCTCCAAC ACATCAGGC

A/G

TGGTCCTCCG GGCCTTTGCA TGGGCTGTTT CTTCCACTTT GCCCAAATGT  
CGCTTTCTCA GGGAGGCCT

20\_106 124

CCACTCTC AAACAGAAAG TTCGGAAGGG AGGCAGGTAA GTGTTAGAAA  
GGCGTTAATG TCATGTT

C/T

CTATCAAACCT GAGACTGCCG CCTAGATGCC ATCAGAATGA TTGACAGAGA  
ATGAAATG

20\_107 147

CCCTTC TCAGAGGGCT ATGTAAACAT TTAAAAAGTT ACTGTAGTAA  
GTTGCTTGGA GGAGTGCCTC ACCCATGCAC TCAATAC

C/T

ACATTCGACA AAGTGATACT GAGGCTTTTC TGTGCCAGGA ACGAGGATAA  
AGATGGTGAA AAA

Table III

20\_109 111  
GGAGT TCCTTTGTGT GAACCTAAAG GATTGATTGA GATGATAAAA T  
A/G  
TCATCGCTGC TCTGACTACG TCTTTGATAT TTGTATGGAA TAATTACATG  
AATAGGTCCA ATGG

20\_110 128  
AGTGCA CGGATTCTAT TAGGGAAATG CGGTGGTAAT TAATGAATCC  
TGCCAGTAAT  
C/T  
GGGAAGGTGT GAGTCCCCGT AATATCGTAA TGATAGTCAT CTGTCTGCGA  
ACCCCCCATC ACTCTGAGAG A

20\_114 137  
CCAAT TTAATTACTT CTTGCTTCTT CTATTATAAG ACACTTATTT  
CCTGGACTGA GAGCCATCTT CAACTCTATC AGCTACTACT  
A/G  
GCTTTTCTCA AGTGACCCAT TCAGCTGTCT CTTCTACCCA CAGTAATGCT  
C

20\_115 143  
AGGTGG CACCTGGCTG TGATCACTGA AAGCACTCTC ACCAGCTGGG  
CTTTCAGCCA AGGTCAGGAC TTTGCACCAC CC  
C/T  
TTCACACATG CCCCAGGCC ATGTCCCAGC AATGCCCTCA GGACCACTGT  
AAAGGAAGCA CAGTG

20\_116 139  
TGA TTCTGAAGTG CTGTGAGGGT CTGAACAGTG GCTGAGGTTT  
ATTTTATAGA ATTTATACGC CTTAAAG  
A/G  
CTGAACTCAG AAATTTGGGA TTCCATTCCC ACATGGCCAT CTAATACAGG  
TATGATCTTG AGAGGTCA

20\_118 128  
CTGGA TGACTTTTTG GCACCGCCTT AAATTCTGTG GCTGAGGCAA  
GTACCTCC  
C/T  
TCGTCATACC CTAATCCTGA CTCTGCACTA AGTACTCAGC ACCCTACAGC  
GATTGAGGCC ATTGCTGTTG TTTT

20\_119 125  
GCCACATGG TGATGCGTGC AGTTAAACAG GAAGCTGGCG GAATGAGTGC  
CTGCGTGGGG A  
C/T  
GGAACAGTTC CGCGTCTCGA GTACAGTGGT GGGGAGATGT GTCTGTGTGT  
GTGATAAAGC TTC

20\_120 136  
GATCATG AAAAGTTTTA AGGAACTCA GAGAAAAAGA GAACAACGCA  
GCTTAAACT TTTAAATGT CCTCCCTCAC CCGTGGCTCA  
G/A  
ACAGCCCTGC ATCTGCCGTG GCCGGCACGT TTCTGGTTGA ACTGCCTT

20\_122 128  
T AAATACAGCC GGAATGATCA ATACACGTGT CCTAAGATCT

Table III

AAGGAGAAGA GCTGTAAGTC ATAA

C/T

GTATGTCCTC AGTGTGGTGC TCCCTCTCCC ATGTTCAATA CTGAGTGTA  
ACTTTTTTTC CA

20\_123 101

ATGAGCA CTCTGCCTTG GTCCCTGGAA GCCTTCCCTG CCATGAGGTT  
GGAGTCAC

A/G

TGGTTCTTCG GTGGGACCCT TAGAATTAGG ATTTAGTGAG CCCAG

20\_124 119

TGTCC ATCATCTCAG AAAGTGCTAC TGGGTAGTAC CGAGGGTCAG GGTG

A/G

CTGCACATCT ACTTTGCTGT GAAACAAGGG CAGATGTAGT TTGGATTGGC  
TAGCCTTCCA GAGTTCTCC

20\_125 147

CTCAAGCGG TCCTCCCTTT TCGGCCTCCC AAAATTCTGG

GATTA

C/T

AGGCGTAAGT CACCATGTTC ATCCAAGAAA TAAATTTTGT GTTGTTTATT  
TGGACTAAGA TATCATCTTA TTTTATCCTA TGAAGGATCT GTTGTAAGCT TC

20\_128 120

AGCGGAGCTG TGGAGAAAGG GCGCAGTGAG CAGAGGGGAC TTGGGCGGT

A/G

AGAATGAAAG AGGGGACGAG GGAGGTTGGG GGTATATGAA TGGAAAAGAG  
TAACGTCGGG GGCAGGACAA

20\_129 101

AA CCACTCTCTC TCCTCTCAAG GGTAGCTCAA GCACTCTCTC  
TTTTCATCAC TCATCT

C/T

GTCTTACTTC ACTACCACTA GTGTTCTAT CTACCTGGAC TC

20\_130 146

CC GGAAAGCTTT GGGCAGCTTG AACAGCTTCC TCCCACCACT  
CTGCACTCCC TGAGCCCAGC AGCCTGCTTC CTGTGAACTT TCTAGAGCAA  
ACGGCCCC

C/T

GTGCAGAAGC AGCATCCACG GCTGAGCAAA CAGGTGGTCA CATGG

20\_131 143

GGCCACAGG CAGTACTGAT AACGCCAAGG TTGCAGTCAG CTAACATCCA  
TTCTCCTATC AGCCAAGGGT CTGGC

A/G

ATAGCCGGGC ACAGGAAGAT TGTGAGTTAT TTCTTCAGGA GGGCTGTGTG  
TCCTGGACAG TGAAGAAG

20\_132 143

CATCAGC CAGGATTGCC GTTACAGTCT TTTTCTCAGG AGCTACAAAG  
ATCTCTTCCT GTTACTAAAT

G/A

GTCGCACCCC AGCAGCCTCT CTCGCACACC GGGGCCCTGC ATGTCAGATG  
GCGTGGTCTG CAGGGGGAGC TCTGT

Table III

22\_001 127  
 AT GCAGATGAAG CCTTCAGGTA GCAGGCTTCC AAGATAACAG  
 GTTGTAATA GTTCTTATCA GACTTAAGTT CTGTGGAGAC  
 A/G  
 TAAATGAGG CATATCTGAC CTCCACTTCC AAAACATCT GAGA

22\_003 147  
 TCT TTCAAAAATG GAAGGGAAAT AAAGACTTTC TCATGTGCAC  
 AAAAGCTGAA AGAGTTCATC  
 G/A  
 CCACTATACC TGCCTTATAA GAAATGCTAA AGGGAGTCCA TCATGTTGAA  
 ATAAAGAAT GCTAGGCAGC AACATCAAAA CAT

22\_004 148  
 CC CTCCTCCTGC TTGGCTCTGT AGCTGTCATT GTCCAAGCTT GGAGGGCTC  
 A/G  
 TGTACAAGCT AACATGGAGG AGGAGCTGGA AGATTGCCTC TCCCGGGGGT  
 CTTGCCTGTT CAGTGGAAAG AAGATGGGAT CATTACAGCC ACTCCA

22\_005 147  
 A CACTCACCT TGCTCTGCTA ATAAGAGGAA GTAGGCGGGG  
 ACGTGGTCAT CACCCTGAGG  
 T/C  
 CCCCACCCA GCTCCTCACA GTGGGAATAA ATGAGCACAG CTCTACAGTG  
 GAGCCAGCAG TCTCGTGACA AGTCTGACAG CAAAG

22\_006 149  
 TC AAGTGTCCCA CCTGCCTTGG CCTCTGAAAG TGCTGGGATT  
 ACAGGCGTGA  
 A/G  
 CCACCATGCC TGCTGGTCTC TGCTTTTTGA ATGCTGACAT GCTGACCTTA  
 GATGTGGGGT AGGGATGATC AGACCAAGTA TTCTGAATTA TGGACT

22\_007 140  
 AGCCG GTTGACTTCC  
 TAGGGCCTTG AGTCACATAC CACCACTCCA GCGCTGGGTG ACTGC  
 A/G  
 GGTGGGTCAT CATGCAGCCT CATTATTCC CCTCACTGGC CTCCAAGGGC  
 TGCTTTGAGA AACCCCTCAC GCAGCACAG

22\_008 143  
 CCCCC AGGCTGACTC AGAGACGTGT CCCTCCACCC GTGTGGCCAT  
 GTGTTGTTCC ATCCTAAAGC TATGGCACAC TCCCATCAT  
 A/G  
 TCCCTCAGTG CAAACCCACC GAGCCCTGTG GTAGGGACGC AGTGTCTAGG  
 AAGGCCTC

22\_015 110  
 T TGGAACCTTA TTACACTTCG AGTCACTGGT TTGCCTGTAT TGTGAAACCA  
 A/G  
 CTGGATCCTG AGATCCCCAA GACAGAAATC ATGATGAGTA TGTTTTTGGC  
 CCATGACA

22\_016 149  
 CCAAATGT CAGGGTCCTG GCACCACAAG GCCTTCCAAG AATAGGAGCC  
 CAGAAGTCCT CATG  
 C/T  
 GCAGTTATAG CAGGTGGAAT TCTACTTTTT TATTGAGGTA CAACTAGCAT

Table III

ACAGTAAAGT GCATAAATCT TAAGTGCATA GCTTG

22\_018 129  
TC ACTGATGGTC ATGCTGGTCT CTTGTTTGTG GAGCAGCAAC  
ATAAAGAAAT TGTACAGTG AAGAAACAG  
C/T  
CACTTTTGGT CAGCCAGGGC AGATGGAAAA AGGGCCTAAC GGGTACACAA  
CGTGAAC

22\_019 132  
TCACAGGACG TCTCCTTCAC AGTGGGTCTG TGCTTCTTTG TGGCCCAGAA  
CAAATTAGTG GGGCTTGGAT TTATGAG  
A/G  
CAGATTCCCC AACCTCTGGA AGGTGTGACT TGCCACAGGG AAAGAAGGCC  
CCTC

22\_020 141  
TCAAGTGA TCCTCCTGCC TCAACCTCCC AAAGTGCTGG GATTACAGGC  
ATGA  
A/G  
CCAGTGCACT TGACCTGATA ATAGGATTCT TTACACTTTA TTATCAGAGT  
GATCTTGAAC CCTTCTGGAA TTGCATAATG TCAGCCCC

22\_021 144  
GAACT CCAAACCTCCT TTCTATTCTT TGTCAGGCAG AAAGCGATTG  
G/A  
CCTGGGCTGG TTAGCCTGGT TCTCATCTCC ATGCTCAAAA GCTATGTCAG  
GCTCCTGGGA AGGGATGCTA TTGATACCTG GCTACTTGCC TAGCTGCT

22\_023 132  
GTGC AGGGCAGAGT CTCAACACAG GAATTGGAAC ATAACAAATC  
T/C  
GCCGACTGCC AGCTTTGATC TCACAAGGAT GGAGTTGGGG AGGTGAAGAG  
AAAGTAAATG CTCTCTCGAC TTTCCAAAGG AAAACAA

22\_024 124  
GGAGAGGGA TGC GGCAAGA GTTAGGAAGT GTCTAGATCC TTGGTTCATT  
TATCAACAAA TGTGAGCCAA ACCA  
C/T  
GTGGTGGGTG CTAGAATACA CCAGCGATAA GAACTGGGAG AACACTGCCT

22\_025 106  
CAATC TTTTCTTTTC TTTCAACAAT CTGTTTCATGC CACAACACT GACTA  
C/T  
ATATCTAGCA CGTATAGGTA CTGTGCTAGA AAGAGAAGCT GGAAGGTGGG  
AATAC

22\_026 102  
TATGTGGT AGGGTGTTAC GTTGGTCAGT TTTTAAGGAT AGTCTACAAG  
ACCATACG  
A/G  
TCTAATGGAA AGAGAGAGCT AGACTGAGAG GTATAATGGC ATTTT

22\_027 127  
GA GCTGTTTGCT ATGGTGGCAG TAGCTGGAGA GCTACTGTTA  
ATTAATTTGA GCAACAGTGC  
A/G

Table III

GCTGATAAAT TTGATCTAGC AGGGAGGTCT GGGACTGCCA TCCTGAACTC  
AAGGTTCTCA AATC

22\_028 120  
AGTAAGGG TAACTTGTCA CTCCTTCACC TACCATGTAA TCCTCATGGG  
CAA  
C/T  
TGTCACCCAT TTCACCAGGC GAGAGACAAC CTTGGCAGGG AAGAGGTACT  
GGCAATCACT GGTAAC TG

22\_029 127  
C GGGGTTTCTC CATGTTGGTC AGGCTGGTCT CAGGTGATAC GCCC  
A/G  
CCTTGCCAC CCGGAGTGCT TGGATTTATA GGCCTGAGCC ACAGCTCCTG  
GCCTAGATTA TAGGTTTAA CATGTGACCC C

22\_030 110  
TGG CTGAGTTAGA  
GTGGTGTAGC ATTGAGCTGC TCAGTTCGTG GCAAGGGTGG GATCACGGCT  
A/G  
AGGCTGCAGA CAGCACCACA GTCTCCCGCT GCGAGGGTCG GTTGGT

22\_031 105  
CT GCCTCTTCCC AAGACTCAGC CACACAAGAC TACTTCCTTC AGGAGA  
C/T  
GTTGGTTTAT GTGCTTAGGG TCTCTGCATG AGAAGTTCCC TGCTTGGGAC  
GTCCCT

22\_032 124  
CA TGGCAGAAAT CAGCAGCTTC CCCTGGGGAT TGTCTACTGA  
GCACCTACAG AACCATATGG G  
C/T  
CTACCAGGAC TGGGACAGTG GCCCAAACA TAGAGGTTCC TGATCGGCTC  
AGGAAC TAGG

22\_033 128  
CT GGAGATAAAG CCTCAGATT TATGACTTAC ATGTGATGAC TGAATGTTCA  
T/C  
GTCCCCATTT GTGTTTCCTA GGGCTGTTAT CACAGATCAC AGCTACAGTA  
AATGTTTACA GCAATTCTGC TGTCC

22\_034 121  
TTAG TATGTCTCCT TCCATCTCAG GCTGTGACAA CCAAAATGT  
CTTCAGACAT TGCCA  
A/G  
ATGTCCCTAG CTGAGAATCA CTAGTTGAGA ACCACTGCTT TAGAATGTAA  
GCGCCTTGAG G

22\_036 124  
TGA TGGGGTGTTT GGAGTTGACA AAGTATCGTA AACACTCATG  
TTAGCGCCTT TGATCTCCA  
C/T  
GAAAGCCTTA AAAGACGGGC AGGATTTCTT CCTTTTTTAT AGGTGAGCAA  
ACAAGGGCAA

22\_037 136  
CA AGATGTAGAG GCACGTGCTT AGGGTCACCC AGCTCAGGCC TGGTAGGAGC

Table III

AGAACC

A/G

GAACCCAGGC CTGCTTCTTT GTTTTATTCA AATCCTATGC ACAACTCAGA  
CAGTTCTACA ATGAATTCAA GCCTGAA

22\_038

124

AG CACCGCAATA CTGACAGTCA ATCTGGTAAT GGATTTGGCT  
GCAAAGTGAC TAACTCAGGT AGCATGTACA G  
C/T  
ATGGATCTAC GGGACAAATG GGATGATCCA CATTCCAGGG TGGACAGAGT

22\_039

141

TGGA GAATTGGGGA CCTTTTAACA ATTTTCTACA AGAACAGTGC CGC  
C/T  
GGTGATGTTG CAGAAGAGAG CTTAGACTTC ATCTATGAAG CCACAGAGCA  
TGGTGTGGAA ATCTGCAGTT AGAAGATGGA TTTTGTGCGA CAG

22\_040

147

TTTG GGAAGTGTG CCAAGCGGGG AGGAAGGGTA TGGAGCAGAT  
CCATGGTGAT CACTGATGCC ACTTTACTCC CTTTCCATTC CC  
A/G  
GAGGAGAGAA ACCATTTTGG AGCTATAGTG ACCTCATTTT ATGGAAAATA  
ATATTTGGCC

22\_041

148

CAGCCCTGA CTGCAACCTC TCTGACCACA GCTCAGAGAG GGCATGTGGC  
ATGCTCACAA ACAGTCTGTT AGGGGCTTCC  
C/T  
CTGGGTCAGA ACTCAGACCC CTCGGCTCTT AGTCCAATGC TCCTCTCCTA  
ACCCAGGTTG CCTTTGGG

22\_042

128

CCC AAATAACCCT ATGAAATAGT TATTATTATT TACATTTACA  
GGTGAGAAA CTGAAGGCTA CAGAATTAAA AGACA  
C/T  
GAAAACAAAG CTCAAAGAGT GAAATGACTT GCCCAAGGGC ATGGGAAGC

22\_043

111

AGGGCTTTG CCACCTGGTT GAGGAGACAG ATACTTGAAA ACAGAGAAGC  
ACAAG  
A/G  
AAGTGTCTGG ATCTTTGCCG ACATCTGAAC TGGCAGAGGC TGCAAATGTC  
TGAGGG

22\_044

126

GGGGGGA GGCAGCCATG CTCTGAGCAC CTGCTCCTCA CCAGGCATT  
C/T  
ACCAGGCACC ATCTCACTTA ATCCTTCCAA GAATCCTAGG CATTACGGGA  
CTTCCATTG AGGCTCAGAG AGGTCCAGT

22\_045

147

TCCTGAGCC AACTTTAAAC ATCTTAAAAG CACTATCACT ATTCCCACTT  
TGCAGATGAG GAAACTGAGG CCTCACAAC GCTAC  
A/G  
CAGTGGCTTC CAGCCTCCAC GGCCCCAGGC TCCGTTCAAG AGCTGCTGTG  
GGATCCTGTT TC

Table III



22\_046 110  
 TTTTA AGTCCCTACA TTTTGGGTTA ATTTATTACG CAGTGATAGA  
 TAACTAATAT ACCTTGCCAA  
 G/A  
 CAATTGTTAT TGGAAGGCTG GTAGACGGAA TAATATTCCT GAAG

22\_047 144  
 AGGTGTGCAC TGTCACCCTC AAGCGGCCTG AGAAGAGGTG GTGCAGCCAG  
 CAGGGGCCAG TCCTG  
 C/T  
 GTTCTTATCC CCCTCTTGTC ACAGATGCCT GCAGAGTGGC TGGTGATGGG  
 GCCTGCGCTT GCTTGCTAAC CAGTCTCT

22\_048 104  
 TGGAAGGC ACAGTCCAGT GAACAGACAG CCATGTGAAC AAA  
 C/T  
 AGATATAGAA TAATTCATTC TACCAATGCT ATGGTAGAGG TGTGGGCAAG  
 ATTCTGGCTC TT

22\_050 133  
 CCCTGC CACTTACTTG CCATATGACT TTGGGCAAAG GACTGAACCC C  
 C/T  
 GCTGAGCACC AGCTTCCTCA CTTATAAAAT GGAGATTAGG ATATTATGGC  
 AATAGTACCT ACCACATAGG ATTATTTTGA GAACT

22\_051 128  
 TTTCCATT TCAATTATCC CTTTCTAAAA CTGGGTCTTA AGCAAACCTGG AATTG  
 A/G  
 GTGTTTCCCA GGTCTCTTCA AACACTTTAA TATGTTGGTT CCCAGACTTC  
 GGTTTCAGGG AACTGTAAGG TTGA

22\_052 132  
 T GAATTATAGA CTTGAACCCT GGACTCTCAC ATTAAAATC TGATGCT  
 C/T  
 GACCAACTGA GCTACACAGA CTTCTAACCA GACTTTTTAT CCCTTTCACA  
 GCAGCATCCC CACATCCCAT GAGTTAATTC TGT

22\_057 149  
 CATGACA GAGACCAGCT CTTGTTCAGT GCCCCCTACC TGCTGGCTGC  
 TTCCTCGGCT CCTCGAACAG ATCAGCCGAG CTTATGGAGG AACTTGC  
 C/T  
 GACAGCCTCT CTAGGCGGGC CCTGGTCTCA TACTAGAGAA GACAAGGAAA  
 AGGA

22\_059 143  
 GGTGGCC CAGCGGGGCA AGAGAGTAAG GACTGGGAGC GAGTGGGACC  
 A/G  
 AGACAAGAGG CCTGGTCCCG CCTTCCTTGA GAGCAGGGCA GGGTGGAAAC  
 CAGCCTCGCT CCTCCTCAGG GGCTGGAATG GAAGCCAGAG AACAG

22\_060 135  
 GAAGCAG CCCCAGCATC AGGGACAGGC CAGGAGTGCA GAATGCATGG  
 AAGCTGGTCA GGTGCGAGCC  
 C/T  
 GGGATGAAGG AAGCACAGAG ATGCAAGGGT GCCAGGGCCC ATGGAACCAA  
 GAGCCGATGA TCAAGGC

22\_062 144

Table III

CTT GCCACATTGC TTGGATGGCC TTTCACCAGG TCTGATCCGA GGGTGGTCTC  
 G/A  
 TCTTTGTCTT AGCAGCCGAG GTCTGTGACC TTGACCACCT GGTGAAGTGT  
 TTGCTGTAAA GTCACCTCTTT TTTCCTTGCT TCCCATACTG

22\_064 112  
 AGT GGTGTGATCA TAGCTCACTG CAGCCTCGTC CTCCTGAGCT  
 CAGCTGATCC TCCAGCCTCA  
 G/A  
 CCTCCTGAGT GGCTGAGACT ATATGTGTAC ACCAGCATGC CTGGCTAA

22\_065 112  
 GACTGG GATGGGCAAG AGGTACGGGA CCTGCTCGGC TCACCTCCCT  
 C/T  
 CTGCAGAGAG ACTCCCAAGG GCTCAGCTGC TCAGAACACT CTAGTTGCC  
 GTGAGGAGCC CAGGG

22\_066 138  
 TGCAAAGAC ACAATAAGCT ACGTATACAT AGTGGTATAC ATATGCACGC  
 ACATACATGC AC  
 A/G  
 TCCACAATCC ATGTTCTAT GCACCTGTTT CTGCCCCATGC AGGTTTCATGC  
 ACACATATTC CCTGCAAATG TTTGTC

22\_067 147  
 GTGAATGGAG ATGGACACAT AGCCCTGGGG TAGTTGGAGC TTTTCCTGGC  
 A/G  
 GTATCCATGG CAACAGGAAG CACAAACAGA AGCATCATTC TACAGCCAAC  
 AAAGAGTTCG TTTTAAAAAT CACCATTATC TTTTCAGAGT GCTTCT

22\_068 135  
 AAGGGCTGAG AGAACTAGAA GAGCCTGATA AGGATCTGGA GAAGAGGCAG  
 CTTCCGACCT TTGATGCCAC AGTCACTCTG  
 C/T  
 GCTACACCTT CATGCAGGGT CCATGCTGTG GCTGATTTCA CAGAGTGGGA  
 TATT

22\_069 145  
 TGGCTCAGTT GCCTGCTTGA GGGGATATTT GTGTCTGTCC CTCATACC  
 A/G  
 GCCACACAAA CCTCCTCAGC CTGGACCACA TGCACGGGTG ACTCCTAGAT  
 CCCTATCTTT GACCTCCATG CCTAGGCACC TGGCATCTTC CAGCAT

Claims

What is claimed is:

1. A method for designing a multiplicity of primers for simultaneous  
5 amplification of a multiplicity of target DNA fragments in a single multiplex polymerase  
chain reaction comprising the steps of:
  - a. aligning a first primer and a second primer; and
  - b. selecting the first primer wherein 1) the first primer at its 3' end does not contain  
four or more bases that are perfectly matching to the 3' end sequence of the first primer or a  
10 second primer; the first primer at its 3' end does not contain seven or more bases that are  
perfectly matching except one mismatch to the 3' end sequence of the first primer or the  
second primer; the first primer at its 3' end does not contain six or more bases that are  
perfectly matching to a sequence anywhere of the first primer or the second primer; and the  
first primer at its 3' end does not contain eleven or more bases that are perfectly matching  
15 except one mismatch to a sequence anywhere of the first primer or the second primer.
2. A method of claim 1 wherein at least 100 primers are designed.
3. A method of claim 2 wherein at least 200 primers are designed.
4. A method of claim 3 wherein at least 1000 primers are designed.
5. A method of claim 1 wherein at least 50 target DNA fragments are produced  
20 in the single multiplex polymerase chain reaction.
6. A method of claim 1 wherein at least 100 target DNA fragments are produced  
in the single multiplex polymerase chain reaction.

7. A method of claim 1 wherein at least 500 target DNA fragments are produced in the single multiplex polymerase chain reaction.

8. A method of claim 1 wherein the single multiplex polymerase chain reaction is used for an application.

5 9. A method of claim 8 wherein the application is selected from the group consisting of an identification of multiple genes related to multifactorial diseases, a genome-scale detection of genetic alterations in cancers, a study in large-scale pharmacogenetic reactions, a genotyping genetic polymorphism in a large population, and a gene expression profiling.

10 10. A method of claim 1 wherein the primers increase the efficacy of the single multiplex polymerase chain reaction.

11. A method of claim 1 wherein the primers minimize the non-specific extension of the single multiplex polymerase chain reaction.

12. A computer product comprising a computer readable medium containing a  
15 computer program which once executed by a computer processor performs the method of claims 1-11.

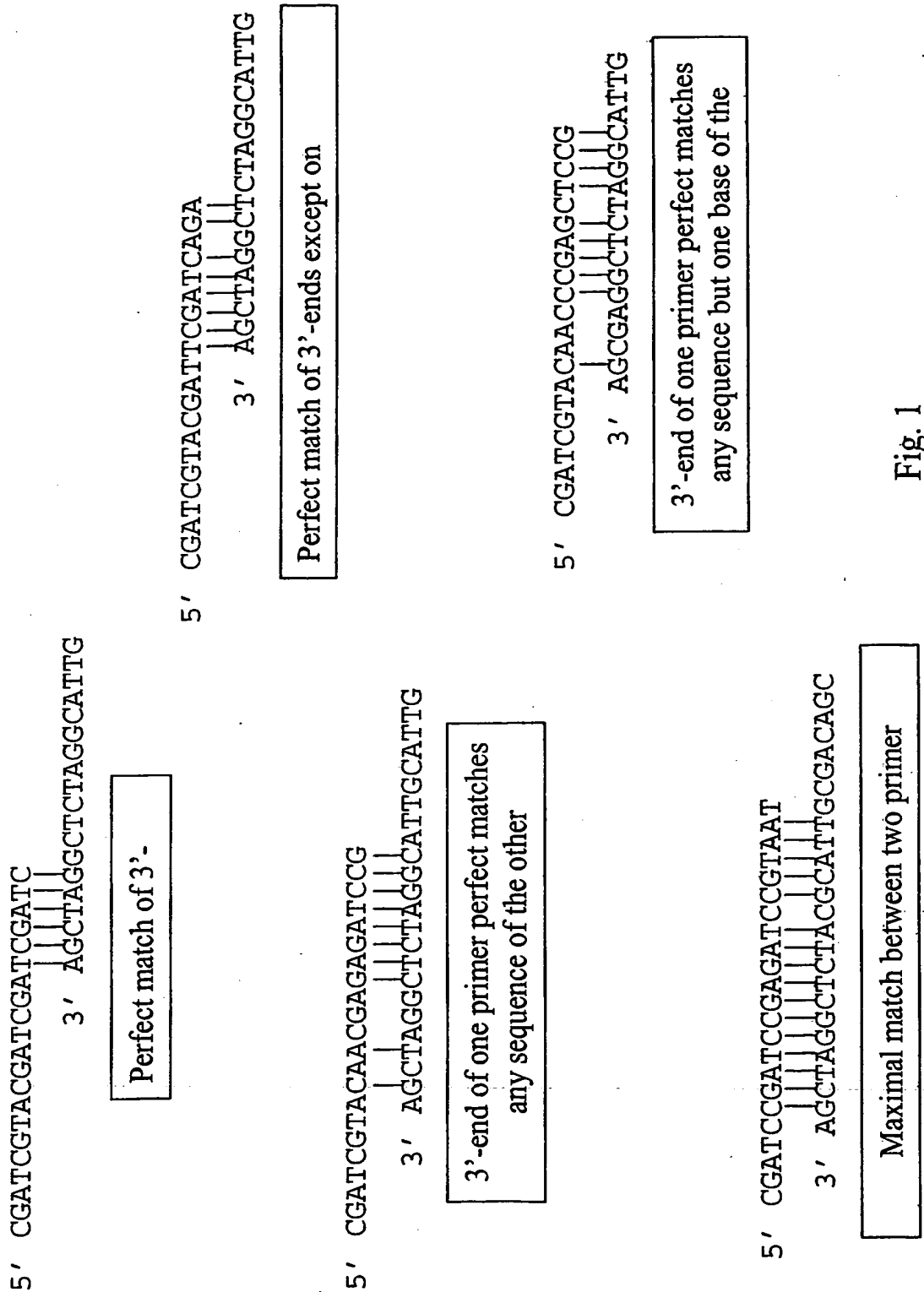


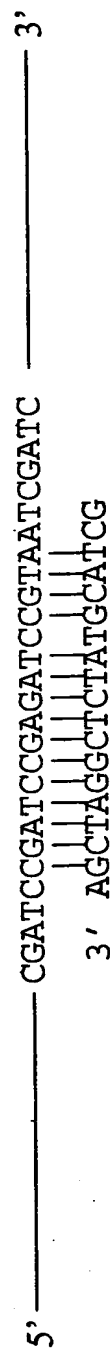
Fig. 1



3'-sequence of a primer perfectly matching a non-specific sequence amplified by other



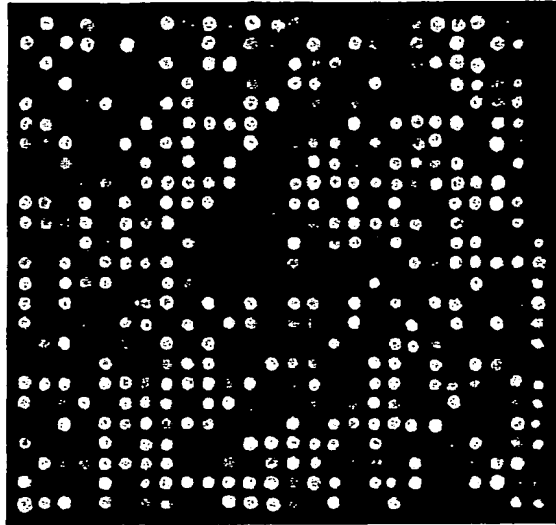
3'-sequence of a primer perfectly matching except one base with a non-specific sequence amplified by other primers



Maximal match between a primer sequence and a non-sequence amplified by other

Fig. 2

Red



Green

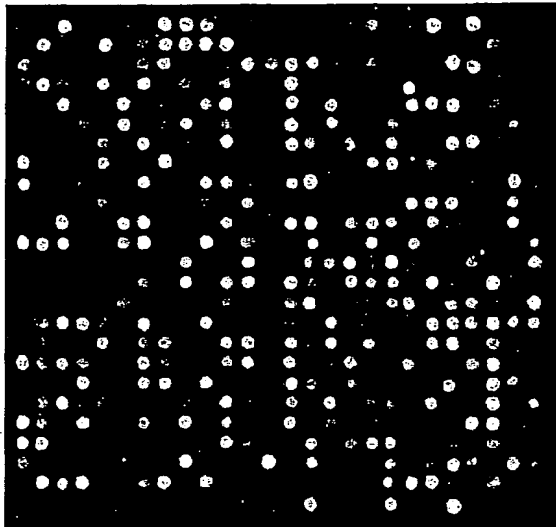


Fig. 3

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Criteria Used in Designing Primers That Are Experimentally Acceptable	
T <sub>m</sub> Range of the primers (°C)	75-103
Length of the primers (bp)	24-33
Number of consecutive matching bases between the 3' ends of any two primer molecules	<4
Number of consecutive matching bases with one mismatch between the 3'-ends of any two primer molecules	<7
Number of consecutive matching bases between the 3'-end of one primer molecule and anywhere in another primer molecule	<9
Number of consecutive matching bases with one mismatch between the 3'-end of one primer molecule and anywhere in another primer molecule	<11
Maximal number of matching bases between two primer molecules	<75%
Number of consecutive matching bases between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	12
Number of consecutive matching bases with one mismatch between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	15
Maximal number of matching bases between a primer molecule and a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	<80%

Fig. 4